Forman
09/308397 Page 1
Seq IDs (#2 w/
Interf.

OM nucleic - nucleic search, using sw model

```
         Copyright   GenCore version 5.1.6
         Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:       June 11, 2003, 17:57:02 ; Search time 2186 Seconds
                                        (without alignments)
                      10592.969 Million cell updates/sec

Title:         US-09-308-397-1
Perfect score: 921
Sequence:      1 atgactaaaacagcctttt.......tagcactttttagaaaatag 921

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

Searched:      24791104 seqs, 1257124 3825 residues

Total number of hits satisfying chosen parameters:       49582208

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Pending_Patents_NA_Main:*
    1:  /cgn2_6/ptodata72/pna/PCTUS_COMB.seq:*      44:  /cgn2_6/ptodata/2/pna/US6000_COMB.seq:*
    2:  /cgn2_6/ptodata/2/pna/US06_COMB.seq:*       45:  /cgn2_6/ptodata/2/pna/US6001_COMB.seq:*
    3:  /cgn2_6/ptodata/2/pna/US07_COMB.seq:*       46:  /cgn2_6/ptodata/2/pna/US6002_COMB.seq:*
    4:  /cgn2_6/ptodata/2/pna/US080_COMB.seq:*      47:  /cgn2_6/ptodata/2/pna/US6003_COMB.seq:*
    5:  /cgn2_6/ptodata/2/pna/US081_COMB.seq:*      48:  /cgn2_6/ptodata/2/pna/US6004_COMB.seq:*
    6:  /cgn2_6/ptodata/2/pna/US082_COMB.seq:*      49:  /cgn2_6/ptodata/2/pna/US6005_COMB.seq:*
    7:  /cgn2_6/ptodata/2/pna/US083_COMB.seq:*      50:  /cgn2_6/ptodata/2/pna/US6006_COMB.seq:*
    8:  /cgn2_6/ptodata/2/pna/US084_COMB.seq:*      51:  /cgn2_6/ptodata/2/pna/US6007_COMB.seq:*
    9:  /cgn2_6/ptodata/2/pna/US085_COMB.seq:*      52:  /cgn2_6/ptodata/2/pna/US6008_COMB.seq:*
   10:  /cgn2_6/ptodata/2/pna/US086_COMB.seq:*      53:  /cgn2_6/ptodata/2/pna/US6009_COMB.seq:*
   11:  /cgn2_6/ptodata/2/pna/US087_COMB.seq:*      54:  /cgn2_6/ptodata/2/pna/US6010_COMB.seq:*
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   16:  /cgn2_6/ptodata/2/pna/US092_COMB.seq:*      59:  /cgn2_6/ptodata/2/pna/US6015_COMB.seq:*
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   19:  /cgn2_6/ptodata/2/pna/US095A_COMB.seq:*     62:  /cgn2_6/ptodata/2/pna/US6018_COMB.seq:*
   20:  /cgn2_6/ptodata/2/pna/US095B_COMB.seq:*     63:  /cgn2_6/ptodata/2/pna/US6019_COMB.seq:*
   21:  /cgn2_6/ptodata/2/pna/US095C_COMB.seq:*     64:  /cgn2_6/ptodata/2/pna/US6020_COMB.seq:*
   22:  /cgn2_6/ptodata/2/pna/US095D_COMB.seq:*     65:  /cgn2_6/ptodata/2/pna/US6021_COMB.seq:*
   23:  /cgn2_6/ptodata/2/pna/US096A_COMB.seq:*     66:  /cgn2_6/ptodata/2/pna/US6022_COMB.seq:*
   24:  /cgn2_6/ptodata/2/pna/US096B_COMB.seq:*     67:  /cgn2_6/ptodata/2/pna/US6023_COMB.seq:*
   25:  /cgn2_6/ptodata/2/pna/US096C_COMB.seq:*     68:  /cgn2_6/ptodata/2/pna/US6024_COMB.seq:*
   26:  /cgn2_6/ptodata/2/pna/US096D_COMB.seq:*     69:  /cgn2_6/ptodata/2/pna/US6025_COMB.seq:*
   27:  /cgn2_6/ptodata/2/pna/US096E_COMB.seq:*     70:  /cgn2_6/ptodata/2/pna/US6026_COMB.seq:*
   28:  /cgn2_6/ptodata/2/pna/US097A_COMB.seq:*     71:  /cgn2_6/ptodata/2/pna/US6027_COMB.seq:*
   29:  /cgn2_6/ptodata/2/pna/US097B_COMB.seq:*     72:  /cgn2_6/ptodata/2/pna/US6028_COMB.seq:*
   30:  /cgn2_6/ptodata/2/pna/US097C_COMB.seq:*     73:  /cgn2_6/ptodata/2/pna/US6029_COMB.seq:*
   31:  /cgn2_6/ptodata/2/pna/US098A_COMB.seq:*     74:  /cgn2_6/ptodata/2/pna/US6030_COMB.seq:*
   32:  /cgn2_6/ptodata/2/pna/US098B_COMB.seq:*     75:  /cgn2_6/ptodata/2/pna/US6031_COMB.seq:*
   33:  /cgn2_6/ptodata/2/pna/US098C_COMB.seq:*     76:  /cgn2_6/ptodata/2/pna/US6032_COMB.seq:*
   34:  /cgn2_6/ptodata/2/pna/US099A_COMB.seq:*     77:  /cgn2_6/ptodata/2/pna/US6033_COMB.seq:*
   35:  /cgn2_6/ptodata/2/pna/US099B_COMB.seq:*     78:  /cgn2_6/ptodata/2/pna/US6034_COMB.seq:*
   36:  /cgn2_6/ptodata/2/pna/US099C_COMB.seq:*     79:  /cgn2_6/ptodata/2/pna/US6035_COMB.seq:*
   37:  /cgn2_6/ptodata/2/pna/US099D_COMB.seq:*     80:  /cgn2_6/ptodata/2/pna/US6036_COMB.seq:*
   38:  /cgn2_6/ptodata/2/pna/US100A_COMB.seq:*     81:  /cgn2_6/ptodata/2/pna/US6037_COMB.seq:*
   39:  /cgn2_6/ptodata/2/pna/US100B_COMB.seq:*     82:  /cgn2_6/ptodata/2/pna/US6038_COMB.seq:*
   40:  /cgn2_6/ptodata/2/pna/US101A_COMB.seq:*     83:  /cgn2_6/ptodata/2/pna/US6039_COMB.seq:*
   41:  /cgn2_6/ptodata/2/pna/US101B_COMB.seq:*     84:  /cgn2_6/ptodata/2/pna/US6040_COMB.seq:*
   42:  /cgn2_6/ptodata/2/pna/US102A_COMB.seq:*     85:  /cgn2_6/ptodata/2/pna/US6041_COMB.seq:*
   43:  /cgn2_6/ptodata/2/pna/US102B_COMB.seq:*
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SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	921	100.0	921	17	US-09-308-397-1	Sequence 1, Appli
	2	913	99.1	921	22	US-09-583-110-1251	Sequence 1251, Ap
	3	913	99.1	921	29	US-09-752-069A-30	Sequence 30, Appli
	4	913	99.1	924	61	US-60-174-089-30	Sequence 30, Appl
	5	913	99.1	924	15	US-09-107-443-794	Sequence 794, App
	6	913	99.1	19702	41	US-10-158-844-7	Sequence 7, Appl
	7	913	99.0	19706	46	US-60-029-960-61	Sequence 61, Appl
c	8	911.4	99.0	921	1	PCT-US02-03997-9442	Sequence 9482, Ap
c	9	911.4	99.0	921	31	US-09-815-242-9482	Sequence 9482, Ap
	10	911.4	99.0	921	39	US-10-072-851-9482	Sequence 9482, Ap
	11	911.4	99.0	3580	1	PCT-US97-22578-43	Sequence 43, Appl
	12	911.4	99.0	9753	50	US-60-068-175-555	Sequence 555, App
	13	908.4	98.6	945	29	US-09-752-069A-256	Sequence 256, App
	14	891.6	96.8	5963	50	US-60-061-998-494	Sequence 494, App
	15	529.4	57.5	547	17	US-09-308-397-5	Sequence 5, Appli
	16	523.2	56.8	1196	12	PCT-US97-07950-8	Sequence 8, Appli
c	17	523.2	56.8	1199	12	US-08-032-030-78	Sequence 78, Appl
c	18	523.2	56.8	1209	16	US-09-297-451-81	Sequence 81, Appl
c	19	523.2	56.8	1209	16	US-09-297-451A-81	Sequence 81, Appl
	20	402	43.6	636	12	US-08-832-030-157	Sequence 157, App
	21	388.8	42.2	927	80	US-60-360-039-42057	Sequence 42057, A

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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22   366     39.7   450      17   US-09-308-397-3       Sequence 3, Appli
23   350.8   38.1   948      15   US-09-134-000-1582    Sequence 1582, Ap
24   344.4   37.4   942      1    PCT-US02-03987-6823   Sequence 6823, Ap
25   344.4   37.4   942      31   US-09-815-242-6823    Sequence 6823, Ap
26   344.4   37.4   942      39   US-10-072-851-6823    Sequence 6823, Ap
27   340.4   37.0   3656     14   US-09-070-927A-577    Sequence 577, App
28   340.4   37.0   3656     14   US-09-070-927-577     Sequence 577, App
29   316.8   34.4   2969     49   US-60-050-444-527     Sequence 527, App
30   316.8   34.4   2969     50   US-60-068-186-533     Sequence 533, App
31   315.2   34.2   987      15   US-09-107-532-3319    Sequence 3319, Ap
32   315.2   34.2   987      15   US-09-107-532A-3319   Sequence 3319, Ap
33   301     32.7   3627     48   US-60-045-649-929     Sequence 929, App
34   301     32.7   3627     48   US-60-046-653-916     Sequence 916, App
35   301     32.7   3627     50   US-60-068-217-803     Sequence 803, App
36   204     22.1   950      36   US-09-974-300-1143    Sequence 1143, Ap
37   204     22.1   960      36   US-09-974-300-1086    Sequence 1086, Ap
38   198.2   21.5   1002     21   US-09-543-681A-3811   Sequence 3811, Ap
39   196.4   21.3   939      1    PCT-US02-03987-6878   Sequence 6878, Ap
40   196.4   21.3   939      31   US-09-815-242-6878    Sequence 6878, Ap
41   196.4   21.3   939      39   US-10-072-851-6878    Sequence 6878, Ap
42 c 196.4   21.3   1830121  8    US-08-426-787-1       Sequence 1, Appli
43 c 196.4   21.3   1830121  22   US-09-557-884-1       Sequence 1, Appli
44 c 196.4   21.3   1830121  25   US-09-643-990A-1      Sequence 1, Appli
45   186.6   20.3   1198     27   US-09-680-598A-74     Sequence 74, Appl
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ALIGNMENTS

RESULT 1
US-09-308-397-1
; Sequence 1, Application US/09308397
; GENERAL INFORMATION:
;   APPLICANT: Gentry, Daniel R.
;   APPLICANT: Lonsdale, John T.
;   APPLICANT: Payne, David J.
;   APPLICANT: Pearson, Stewart C.
;   APPLICANT: Van Aller, Glenn
;   TITLE OF INVENTION: Novel FabD
;   FILE REFERENCE: P50593
;   CURRENT APPLICATION NUMBER: US/09/308,397
;   CURRENT FILING DATE: 1999-05-18
;   EARLIER APPLICATION NUMBER: US 60/031,160
;   EARLIER FILING DATE: 1996-11-18
;   EARLIER APPLICATION NUMBER: PCT/US97/20992
;   EARLIER FILING DATE: 1997-11-14
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Streptococcus pneumoniae
US-09-308-397-1

  Query Match   100.0%; Score 921; DB 17; Length 921;
  Best Local Similarity   100.0%; Pred. No. 2.4e-271;
  Matches   921; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 ATGACTAAAAACAGCCCTTTATTTGTGCTGCAAGGTGCCCAGTATCCAGGATGGGGACGG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ATGACTAAAAACAGCCCTTTATTTGTGCTGCAAGGTGCCCAGTATCCAGGATGGGGACGG 60

Qy   61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGTGCTC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGTGCTC 120

Qy  121 GGTTATGATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 GGTTATGATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 180

Qy  181 ACGCAACCAGCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAGGGC 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ACGCAACCAGCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAGGGC 240

Qy  241 TATCGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCGTCTTGGTGGCAAGC 300
          |||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  241 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCGTCTTGGTGGCAAGC 300

Qy  301 GGGCCTTGGATTTGAAGATGCGGTTGCCTTGGTTGCCTTGGTGAGCGCCATATGGAA 360
          |||||||||||||||||||||||| ||||||||||||||| ||||||||||||||||
Db  301 GGGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTTGCCTTGGTGGAGCGCCTATATGGAA 360

Qy  361 GAAGCGGCTCCTGCTGACTCTGCCAAGGTCAGTTCTCAATACGGTAGAGTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  361 GAAGCGGCTCCTGCTGACTCTGCCAAGGTCAGTTCTCAATACGGTAGAGTC 420

Qy  421 ATTGAAGAGCCTCTCAAAAGCTTCTGGAGAGTTGGTTCAGTGGTTACTCCAGCCAACTATAAC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  421 ATTGAAGAGCCTCTCAAAAGCTTCTGGAGAGTTGGTTCAGTGGTTACTCCAGCCAACTATAAC 480

Qy  481 ACACCTGCACAAATCGTCATTGTGCTTGGAGAGTGGTTGCAGTTGTGCAGGCGGTTGAACTT 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  481 ACACCTGCACAAATCGTCATTGTGCTTGGAGAGTGGTTGCAGTTGTGCAGGCGGTTGAACTT 540

Qy  541 TTGCAAGAGCAGGTGCCAAACGTTGATTCCTTTAAGGTGTCAGGTGTCAGGTCCCTTTCACACC 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  541 TTGCAAGAGCAGGTGCCAAACGTTGATTCCTTTAAGGTGTCAGGTGTCAGGTCCCTTTCACACC 600

Qy  601 GCTCTCCTTGAGCCTGCTGCTAGCTCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAATACAGAGAGGACATT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  601 GCTCTCCTTGAGCCTGCTGCTAGCCAGAAACTGAAACCTCAGCTCAGTGAAGTTTTCA 660

Qy  661 GATTTACTTGTCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAATACAGAGAGGACATT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  661 GATTTACTTGTCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAATACAGAGAGGACATT 720

Qy  721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTCTTCATGAAAGTATTGGGGTC 780
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTCTTCATGAAAGTATTGGGGTC 780

Qy  781 ATGCAAGAGCAGGCATAAGCAACTTATCGACCGGGGAAGTCTGTCAGT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db  781 ATGCAAGAGCAGGCATAAGCAACTTTATCGACCGGGGAAGTCTGTCAGT 840

Qy  841 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTA 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA 900

Qy  901 GTAGCACTTTAGAAAATAG 921
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Db  901 GTAGCACTTTAGAAAATAG 921
```

RESULT 2
US-09-583-110-1251
; Sequence 1251, Application US/09583110
; GENERAL INFORMATION:
;   APPLICANT: Lynn Doucette-Stamm et al.
;   TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;   TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
;   FILE REFERENCE: PATH00-07A
;   CURRENT APPLICATION NUMBER: US/09/583,110
;   CURRENT FILING DATE: 2000-05-26
;   PRIOR APPLICATION NUMBER: US 09/107,433
;   PRIOR FILING DATE: 1998-06-30
;   PRIOR APPLICATION NUMBER: US 60/085,131
;   PRIOR FILING DATE: 1998-05-12
;   PRIOR APPLICATION NUMBER: US 60/051,553
;   PRIOR FILING DATE: 1997-07-02
;   NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1251
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Streptococcus pneumoniae
US-09-583-110-1251

Query Match   99.1%; Score 913; DB 29; Length 921;
Best Local Similarity   99.5%; Pred. No: 7e-269;
Matches 916; Conservative   0; Mismatches   5; Indels   0; Gaps   0;

Qy   1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60

Qy   61 GATTTCTATGATCAGTAGTATCTCATCGATCGGAAGAACGATTGATCGAGCGAGTCAGGTGCTC 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATTTCTATGATCAGTAGTATCTCATCGATCGGAAGAACGATTGATCGAGCGAGTCAGGTGCTC 120

Qy 121 GGTTATGATTACGTTATCATCGATCGGAAGAGACAAACTCAATCAGACCCGCTAT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GGTTATGATTTGCGTTATCATCGATCGGAAGAGACAAACTCAATCAGACCCGCTAT 180

Qy 181 ACGCAACCAGCCATTCGGTTGTCTATCTACCGTTTATTGCAAGAAAAGGGC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ACGCAACCAGCCATTCGGTTGTCTATCTACCGTTTATTGCAAGAAAAGGGC 240

Qy 241 TATCAGCCTGATATGGTTGCTGGTTGTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TATCAGCCTGATATGGTTGCTGGTTGTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300

Qy 301 GGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360

Qy 361 GAAGCGGCTCCTGCGACTTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GAAGCGGCTCCTGCGACTTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 420

Qy 421 ATTGAAGAAGCCTGTCAAAAAGCTTCGAGTGTTACTCCAGCCAACTATAAC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 ATTGAAGAAGCCTGTCAAAAAGCTTCGAGTGTTACTCCAGCCAACTATAAC 480

Qy 481 ACACCTGCACAAATCGTCATTGCTGGTTGCAGTTGATCGAGCGGTTGAACTT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 ACACCTGCACAAATCGTCATTGCTGGTTGCAGTTGATCGAGCGGTTGAACTT 540

Qy 541 TTGCAAGAAGCAGGTGCCAAAGCTTCTCTTAAGGTGTCCCTTCACACC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TTGCAAGAAGCAGGTGCCAAAGCTTCTCTTAAGGTGTCCCTTCACACC 600

Qy 601 GCTCTCCTTGAGCCGTCTGCAGCCAGAAACTAGCTTCAGCCAGTAAGTTTTTCA 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 GCTCTCCTTGAGCCGTCTGCAGCCAGAAACTAGCTTCAGCCAGTAAGTTTTTCA 660

Qy 661 GATTTTACTTGTCCCCAGTCGGCAATACGAAGCTGCTGATGCAAAAAGAGGACATT 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 GATTTTACTTGTCCCCAGTCGGCAATACGAAGCTGCTGATGCAAAAAGAGGACATT 720

RESULT 3
US-09-752-069A-30
;   Sequence 30, Application US/09752069A
;   GENERAL INFORMATION:

Query Match   99.1%; Score 913; DB 22; Length 921;
Best Local Similarity   99.5%; Pred. No: 7e-269;
Matches 916; Conservative   0; Mismatches   5; Indels   0; Gaps   0;

Qy   1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60

Qy   61 GATTTCTATGATCAGTAGTATCTCATCGATCGGAAGAACGATTGATCGAGCGAGTCAGGTGTC 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATTTCTATGATCAGTAGTATCTCATCGATCGGAAGAACGATTGATCGAGCGAGTCAGGTGCTC 120

Qy 121 GGTTATGATTACGTTATCATCGATCGGAAGAGACAAACTCAATCAGACCCGCTAT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 GGTTATGATTTGCGTTATCATCGATCGGAAGAGACAAACTCAATCAGACCCGCTAT 180

Qy 181 ACGCAACCAGCCATTCGGTTGTCTATCTACCGTTTATTGCAAGAAAAGGGC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 ACGCAACCAGCCATTCGGTTGTCTATCTACCGTTTATTGCAAGAAAAGGGC 240

Qy 241 TATCAGCCTGATATGGTTGCTGGTTGTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 TATCAGCCTGATATGGTTGCTGGTTGTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300

Qy 301 GGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 GGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360

Qy 361 GAAGCGGCTCCTGCGACTTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361 GAAGCGGCTCCTGCGACTTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 420

Qy 421 ATTGAAGAAGCCTGTCAAAAAGCTTCGAGTGTTACTCCAGCCAACTATAAC 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 421 ATTGAAGAAGCCTGTCAAAAAGCTTCGAGTGTTACTCCAGCCAACTATAAC 480

Qy 481 ACACCTGCACAAATCGTCATTGCTGGTTGCAGTTGATCGAGCGGTTGAACTT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 481 ACACCTGCACAAATCGTCATTGCTGGTTGCAGTTGATCGAGCGGTTGAACTT 540

Qy 541 TTGCAAGAAGCAGGTGCCAAAGCTTCTCTTAAGGTGTCCCTTCACACC 600
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db 541 TTGCAAGAAGCAGGTGCCAAAGCTTCTCTTAAGGTGTCCCTTCACACC 600

Qy 601 GCTCTCCTTGAGCCGTCTGCAGCCAGAAACTAGCTTCAGCCAGTAAGTTTTTCA 660
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 601 GCTCTCCTTGAGCCGTCTGCAGCCAGAAACTAGCTTCAGCCAGTAAGTTTTTCA 660

Qy 661 GATTTTACTTGTCCCCAGTCGGCAATACGAAGCTGCTGATGCAAAAAGAGGACATT 720
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 661 GATTTTACTTGTCCCCAGTCGGCAATACGAAGCTGCTGATGCAAAAAGAGGACATT 720

Qy 721 GCTCAGCTCTTGACGGGTCAGGTCAAGGTCAACCCGTTCGTTCGTTCGTTCATGAAAGTATTGGGGTC 780
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 721 GCTCAGCTCTTGACGGGTCAGGTCAAGGTCAACCCGTTCGTTCGTTCGTTCATGAAAGTATTGGGGTC 780

Qy 781 ATGCAAGAAGCAGGCAGGCCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGT 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 781 ATGCAAGAAGCAGGCAGGCCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGT 840

Qy 841 TTTGTTAAAAAAAATTGATCAAACTGCTCACTTAGCTCACTTAGCTCACTTCATGTGAAGATCAAGCGAGTTA 900
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 841 TTTGTTAAAAAAAATTGATCAAACTGCTCACTTAGCTCACTTAGCTCACTTCATGTGAAGATCAAGCGAGTTA 900

Qy 901 GTAGCACTTTTAGAAAAATAG 921
        |||||||||||||||||||||
Db 901 GTAGCACTTTTAGAAAAATAG 921

Qy 421 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 480

Db 481 ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATGAGCGGTTGAACTT 540
Qy 481 ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATGAGCGGTTGAACTT 540

Db 541 TTGCAAGAGCAGGTGCCAAACGTTGATTCCTCTTAAGGTGTCAGGTCCCTTCACACC 600
Qy 541 TTGCAAGAGCAGGTGCCAAACGTTGATTCCTCTTAAGGTGTCAGGTCCCTTCACACC 600

Db 601 GCTCTCCTTGAGCCTGCTAGCCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTCA 660
Qy 601 GCTCTCCTTGAGCCTGCTAGCCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTCA 660

Qy 661 GATTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT 720
Db 661 GATTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT 720

Qy 721 GCTCAGCTCTTGACGCGTCAGTCAAGGAACCCGTTCGTTCTTCATGAAGAAGTATTGGGGTC 780
Db 721 GCTCAGCTCTTGACGCGTCAGTCAAGGAACCCGTTCGTTCTTCATGAAGAAGTATTGGGGTC 780

Qy 781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT 840
Db 781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT 840

Qy 841 TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGAAGATCAAGCGAGTTTA 900
Db 841 TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGAAGATCAAGCGAGTTTA 900

Qy 901 GTAGCACTTTTAGAAAAATAG 921
Db 901 GTAGCACTTTTAGAAAAATAG 921

Qy 721 GCTCAGCTCTTGACGCGTCAGTCAAGGAACCCGTTCGTTCTTCATGAAGAAGTATTGGGGTC 780
Db 721 GCTCAGCTCTTGACGCGTCAGTCAAGGAACCCGTTCGTTCTTCATGAAGAAGTATTGGGGTC 780

Qy 781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT 840
Db 781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT 840

Qy 841 TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGAAGATCAAGCGAGTTTA 900
Db 841 TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGAAGATCAAGCGAGTTTA 900

Qy 901 GTAGCACTTTTAGAAAAATAG 921
Db 901 GTAGCACTTTTAGAAAAATAG 921

Query Match 99.1%; Score 913; DB 61; Length 921;
Best Local Similarity 99.5%; Pred. No. 7e-269;
Matches 916; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGACTAAAACAGACCCTTTTATTTGCTGGTCAAGGTGCCCAGTATCCTAGGGATGGGACGG 60
Db 1 ATGACTAAAACAGACCCTTTTATTTGCTGGTCAAGGTGCCCAGTATCCTAGGGATGGGACGG 60

Qy 61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
Db 61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120

Qy 121 GGTTATGATTTACGTATGGTTGCTCGTTTGTCTCTTCTTGGAGAATACTCTCGCCTTGGTGGCAAGC 180
Db 121 GGTTATGATTTACGTATGGTTGCTCGTTTGTCTCTTCTTGGAGAATACTCTCGCCTTGGTGGCAAGC 180

Qy 181 ACGGCAACCAGCCATTCGAGCGACTTCGGTTGCTCGTATCGTGCAAGAAAAGGGC 240
Db 181 ACGGCAACCAGCCATTCGAGCGACTTCGGTTGCTCGTATCGTGCAAGAAAAGGGC 240

Qy 241 TATCAGCCTGATATGGTTGCTCGGTTTGTCTCTTGGAGAATACTCTCGCCTTGGTGGCAAGC 300
Db 241 TATCAGCCTGATATGGTTGCTCGGTTTGTCTCTTGGAGAATACTCTCGCCTTGGTGGCAAGC 300

Qy 301 GGCGGCGGCTCCTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
Db 301 GGCGGCGGCTCCTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360

Qy 361 GAAGCGGCGCTCCTGCTGACTCCTGGCAAGATGGTAGCAGTTCCAATACGCCAGTAGAGGTC 420
Db 361 GAAGCGGCGCTCCTGCTGACTCCTGGCAAGATGGTAGCAGTTCCAATACGCCAGTAGAGGTC 420

Qy 421 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 480

```
LENGTH: 924 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
  NAME/KEY: misc feature
  LOCATION: (B) LOCATION 1...924
SEQUENCE DESCRIPTION: SEQ ID NO: 794:
US-09-107-433-794

Query Match        99.1%;   Score 913;  DB 15;  Length 924;
Best Local Similarity  99.5%;   Pred. No. 7e-269;
Matches 916;  Conservative  0;  Mismatches  5;  Indels  0;  Gaps  0;

Qy    1 ATGACTAAAACAGCCTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4 ATGACTAAAACAGCCTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG  63

Qy   61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 GATTTCTATGATCAGTATCCGATTGTTAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 123

Qy  121 GGTTATGATTACGTTATCTCATCGATACGGAAGGAAGACAAACTCAATCAGACCCGCTAT 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124 GGTTATGATTTGCGTTATCTCATCGATACGGAAGGAGAGACAAACTCAATCAGACCCCTAT 183

Qy  181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTTGCTATCTACCGTTTATTGCAAGAAAGGGC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  184 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTTGCTATCTACCGTTTATTGCAAGAAAGGGC 243

Qy  241 TATCAGCCTGATATGGTTGCTGGTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  244 TATCAGCCTGATATGGTTGCTGGTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 303

Qy  301 GGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCGGTGGAGCCTAGTATGGAA 360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  304 GGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCGGTGGAGCCTAGTATGGAA 363

Qy  361 GAAGCGGCTCCTGCGACTCTGCAAGATGGCAGTTCCAATACGCCCAGTAGAGGTC 420
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  364 GAAGCGGCTCCTGCGACTCTGCAAGATGGCAGTTCCAATACGCCCAGTAGAGGTC 423

Qy  421 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  424 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 483

Qy  481 ACACCTGCACAAATCGTCATTGCTGGAGGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  484 ACACCTGCACAAATCGTCATTGCTGGAGGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT 543

Qy  541 TTGCAAGAAGCAGGTGCCAAACGCTGATTCCTCCTTAAGGTGTCAGGTCCCTTCCACACC 600
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  544 TTGCAAGAAGCAGGTGCCAAACGCTGATTCCTCCTTAAGGTGTCAGGTCCCTTCCACACC 603

Qy  601 GCTCTCCTTGAGCCTGCTAGCCAGCAGAAACTAGCTGAAACTCAGGTTAAGTTTTCA 660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  604 GCTCTCCTTGAGCCTGCTAGCCAGCAGAAACTAGCTGAAACTCAGGTTAAGTTTTCA 663

Qy  661 GATTTTACTTGTCCCCAGTCGGCAATACAGAGCTGCTGTGATGCAAAAAGAGGACATT 720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  664 GATTTTACTTGTCCCCAGTCGGCAATACAGAGCTGCTGTGATGCAAAAAGAGGACATT 723

Qy  721 GCTCAGTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTCGTCATGTATTGGGGTC 780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  724 GCTCAGTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTCGTCATGTATTGGGGTC 783

Qy  781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT 840
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RESULT 6
US-10-158-844-7/c
; Sequence 7, Application US/10158844
; GENERAL INFORMATION:
;  APPLICANT: Kunsch et al.
;  TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
;  NUMBER OF SEQUENCES: 391
;  CORRESPONDENCE ADDRESS:
;    ADDRESSEE: Human Genome Sciences, Inc.
;    STREET: 9410 Key West Avenue
;    CITY: Rockville
;    STATE: Maryland
;    COUNTRY: USA
;    ZIP: 20850
;  COMPUTER READABLE FORM:
;    MEDIUM TYPE: CD-R
;    COMPUTER: Dell Latitude Pentium 3
;    OPERATING SYSTEM: Windows 98
;    SOFTWARE: ASCII Text
;  CURRENT APPLICATION DATA:
;    APPLICATION NUMBER: US/10/158,844
;    FILING DATE: 03-Jun-2002
;    CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;    APPLICATION NUMBER: US 08/961,527
;    FILING DATE: 1997-10-30
;    APPLICATION NUMBER: US 60/029,960
;    FILING DATE: 1996-10-31
;  ATTORNEY/AGENT INFORMATION:
;    NAME: Hyman, Mark J.
;    REGISTRATION NUMBER: 46,789
;    REFERENCE/DOCKET NUMBER: PB340P1D1
; INFORMATION FOR SEQ ID NO: 7:
;  SEQUENCE CHARACTERISTICS:
;    LENGTH: 19702 base pairs
;    TYPE: nucleic acid
;    STRANDEDNESS: double
;    TOPOLOGY: linear
;  SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-158-844-7

Query Match        99.1%;   Score 913;  DB 41;  Length 19702;
Best Local Similarity  99.5%;   Pred. No. 2.9e-268;
Matches 916;  Conservative  0;  Mismatches  5;  Indels  0;  Gaps  0;

Qy      1 ATGACTAAAACAGCCTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG    60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17149 ATGACTAAAACAGCCTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 17090

Qy     61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17089 GATTTCTATGATCAGTATCCGATTGTTAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 17030

Qy    121 GGTTATGATTACGTTATCTCATCGATACGGAAGGAAGACAAACTCAATCAGACCCGCTAT  180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17029 GGTTATGATTTGCGTTATCTCATCGATACGGAAGGAGAGACAAACTCAATCAGACCCGCTAT 16970

Qy    181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTTGCTATCTACCGTTTATTGCAAGAAAGGGC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16969 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTTGCTATCTACCGTTTATTGCAAGAAAGGGC 16910

Qy    241 TATCAGCCTGATATGGTTGCTGGTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC  300
```

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 19706 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-60-029-960-61:

Query Match   99.1%; Score 913; DB 46; Length 19706;
Best Local Similarity 99.5%; Pred. No. 2.9e-268;
Matches 916; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      1 ATGACTAAAACAGCCTTTTTATTTGTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG    60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17155 ATGACTAAAACAGCCTTTTTATTTGTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 17096

Qy     61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACAGATTGATCGAGCGAGTCAGGTGCTC   120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17095 GATTTCTATGATCAGTATCCGATTGTAAAGAAACAGATTGATCGAGCGAGTCAGGTGCTC 17036

Qy    121 GGTTATGATTTACGTTATCTCATCGATACGGAAGAGACAAACTCAATCAGACCCGCCTAT   180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17035 GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGACAAACTCAATCAGACCCGCCTAT 16976

Qy    181 ACGGAACCAGCCATTCTAGCGACTTCGGTTGTGTCTTGGAATATCTCGCCTTGGTGGCAAGC   240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16975 ACGGAACCAGCCATTCTAGCGACTTCGGTTGCTCGTTTGTCTCTTGGAATATCTCGCCTTGGTGGCAAGC 16916

Qy    241 TATCAGCCTGATATGGTTGCTGGTTTGAAGATGCGGTTGCCTGGTAGCTAAGCGTGGAGC   300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16915 TATCAGCCTGATATGGTTGCTCGTTTGTCTCTTGGAGCGTGGTAGCTAAGCGTGGCAAGT 16856

Qy    301 GGCGGCCTTGGATTTTGAAGATGCGGTTGCCTGGTAGCTAAGCGTGGAGCCTATATGGAA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16855 GGCGGCCTTGGATTTTGAAGATGCGGTTGCCTGGTAGCTAAGCGTGGAGCCTATATGGAA 16796

Qy    361 GAAGCGGCTCCTGCTGACTCCTGCGCAAGATGGTTACTCCAGCCAACTATAAC   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16795 GAAGCGGCTCCTGCTGACTCCTGCGCAAGATGGTTACTCCAGCCAACTATAAC 16736

Qy    421 ATTGAAGAGAGCTGCTGTCAAAAAGCTTCTGAGAAAGCTTCTGAGAAGTGGTTACTCCAGCCAACTATAAC   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16735 ATTGAAGAGAGCTGCTGTCAAAAAGCTTCTGAGAAAGCTTCTGAGAAGTGGTTGAACTT 16676

Qy    481 ACACCTGCACAAATCGTCATTGCTGCAGAAGCGGTTGCAGTTGATCGAGCGGTTGAACTT   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16675 ACACCTGCACAAATCGTCATTGCTGCAGAAGCGGTTGCAGTTGATCGAGCGGTTGAACTT 16616

Qy    541 TTGCAAGAGAGCAGGTGCCAAACGTCCCTTTCAGGTGTCAGGTCCCTTTCACACC   600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16615 TTGCAAGAGAGCAGGTGCCAAACGTCCCTTTCAGGTGTCAGGTCCCTTTCACACC 16556

Qy    601 GCTCTCCTTGAGCCTGCTAGCCAGAAACTGCTGTGATGAAACTCTAGCTCAGGTAAGTTTTTCA   660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16555 GCTCTCCTTGAGCCTGCTAGCCAGAAACTGCTGTGATGAAACTCTAGCTCAGGTAAGTTTTTCA 16496

Qy    661 GATTTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATCAAAAGAGAGACATT   720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16495 GATTTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGAGACATT 16436

Qy    721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC   780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16435 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC 16376

Qy    781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT   840
            |||||||||||||||||||||||||||||||||||||
Db
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(left column continued)

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Db  16909 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGT 16850

Qy    301 GGCGGCCTTGGATTTTGAAGATGCGGTTGCCTGGTAGCTAAGCGTGGAGCCTATATGGAA   360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16849 GGCGGCCTTGGATTTTGAAGATGCGGTTGCCTGGTAGCTAAGCGTGGAGCCTATATGGAA 16790

Qy    361 GAAGCGGCTCCTGCTGACTCCTGCGCAAGATGTAGCAGTTCTCAATACGGCCAGTAGAGGTC   420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16789 GAAGCGGCTCCTGCTGACTCCTGCGCAAGATGTAGCAGTTCTCAATACGGCCAGTAGAGGTC 16730

Qy    421 ATTGAAGAGAGCTGCTGTCAAAAAGCTTCTGAGTTGGTTACTCCAGCCAACTATAAC   480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16729 ATTGAAGAGAGCTGCTGTCAAAAAGCTTCTGAGTTGGTTACTCCAGCCAACTATAAC 16670

Qy    481 ACACCTGCACAAATCGTCATTGCTGCAGAAGCGGTTGCAGTTGATCGAGCGGTTGAACTT   540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16669 ACACCTGCACAAATCGTCATTGCTGCAGAAGCGGTTGCAGTTGATCGAGCGGTTGAACTT 16610

Qy    541 TTGCAAGAGAGGTGCCAAACGTCCAAACGTCCCTCTTAAGGTGTCAGGTCCCTTTCACACC   600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16609 TTGCAAGAGAGGTGCCAAACGTCCAAACGTCCCTCTTAAGGTGTCAGGTCCCTTTCACACC 16550

Qy    601 GCTCCTTCCTGAGCCTGCTAGCCAGAAACTGCTGAAACTCTAGCTGAAACTCAGGTAAGTTTTTCA   660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16549 GCTCCTTCCTGAGCCTGCTAGCCAGAAACTGCTGAAACTCTAGCTGAAACTCAGGTAAGTTTTTCA 16490

Qy    661 GATTTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGAGGACATT   720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16489 GATTTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGAGGACATT 16430

Qy    721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC   780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16429 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC 16370

Qy    781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGATCAAAACTGCTCACTTAGCTCAAAAACTGCTCACTTAGCTCAGGTCTTGTCAGGT   840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16369 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGATCAAAACTGCTCACTTAGCTCAAAAACTGCTCACTTAGCTCAGGTCTTGTCAGGT 16310

Qy    841 TTTGTTAAAAAATTGATCAAAACTGCTGGAAGATCAAGCCAGTTTA   900
            ||||||||||||||||||||||||||||||||||||||||||||||
Db  16309 TTTGTTAAAAAATTGATCAAAACTGCTGGAAGATCAAGCCAGTTTA 16250

Qy    901 GTAGCACTTTTAGAAAAATAG 921
            |||||||||||||||||||||
Db  16249 GTAGCACTTTTAGAAAAATAG 16229
```

RESULT 7
US-60-029-960-61/c
; Sequence 61, Application US/60029960
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 1649
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/029,960
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```
Db   16375 ACAACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     481 ACAACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT

Qy     841 TTGCAAGAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGTGTCCTTTCACACC  600
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TTGCAAGAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGTGTCCTTTCACACC  600

Db     601 GCTCTCCTTGAGCCTGCTAGCCAGAAACTAGCTGAAACTCAGCTCAGTAAGTTTTCA    660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     601 GCTCTCCTTGAACCTGCTAGCCAGAAACTAGCTGAAACTCAGCTCAGTAAGTTTTCA    660

Qy     661 GATTTTACTTGTCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAAAAAGAGGACATT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GATTTTACTTGTCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAAAAAGAGGACATT  720

Db     721 GCTCAGCTCTTGAGCGTCAGGTCAAGGAACCCGTTCGTTCATGAAAGTATTGGGGTC    780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTCATGAAAGTATTGGGGTC    780

Qy     781 ATGCAAGAAGCAGGCATAAGCAACTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATGCAAGAAGCAGGCATAAGCAACTTATCGAGATTGGACCGGGGAAAGTTTTGTCAGGT  840

Db     841 TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     841 TTTGTTAAAAAAATTGATCGAACTGCTCACTTAGCTCATGTGGAAGATCAAGCAAGCGAGTTTA  900

Qy     901 GTAGCACTTTTAGAAAAATAG  921
           |||||||||||||||||||||
Db     901 GTAGCACTTTTAGAAAAATAG  921
```

```
RESULT 9
US-09-815-242-9482
; Sequence 9482, Application US/09815242
; GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT: Ohlsen, Kari L.
;  APPLICANT: Zyskind, Judith W.
;  APPLICANT: Wall, Daniel
;  APPLICANT: Trawick, John D.
;  APPLICANT: Carr, Grant J.
;  APPLICANT: Yamamoto, Robert T.
;  APPLICANT: Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;     Prokaryotes
; FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9482
;  LENGTH: 921
;  TYPE: DNA
;  ORGANISM: Streptococcus pneumoniae
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(921)
US-09-815-242-9482
```

```
Db   16315 TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCAAGCGAGTTTA  16256
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     841 TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA  900

Qy     901 GTAGCACTTTTAGAAAAATAG  921
           |||||||||||||||||||||
Db   16255 GTAGCACTTTTAGAAAAATAG  16235
```

```
RESULT 8
PCT-US02-03987-9482
; Sequence 9482, Application PC/TUS0203987
; GENERAL INFORMATION:
;  APPLICANT: Elitra Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
;  TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELITRA.028VPC
;  CURRENT APPLICATION NUMBER: PCT/US02/03987
;  CURRENT FILING DATE: 2002-02-02
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  NUMBER OF SEQ ID NOS: 15811
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9482
;  LENGTH: 921
;  TYPE: DNA
;  ORGANISM: Streptococcus pneumoniae
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(921)
PCT-US02-03987-9482

Query Match             99.0%;  Score 911.4;  DB 1;  Length 921;
Best Local Similarity   99.3%;  Pred. No. 2.2e-268;
Matches   915;  Conservative  0;  Mismatches   6;  Indels   0;  Gaps   0;

Qy       1 ATGACTAAAACAGCCTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGACTAAAACAGCCTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60

Qy      61 GATTTCTATGATCAGTATCCGATTGTCAAGAAACGATTGATCGAGCGAGTCAGGTGCTC  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GATTTCTATGATCAGTATCCGATTGTCAAGAAACGATTGATCGACGGAGTCAGGTGCTA  120

Qy     121 GGTTATGATTTACGTTATCTCATCGATACGGAAGAGACAAACTCAATCAGACCGCTAT  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGACAAACTCAATCAGACCGCTAT  180

Qy     181 ACGCAACCAGCCATTCTCAGCGACTTCGGTTGCTATCTACCGTTATTGCAAGAAAAGGGC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ACGCAACCAGCCATTCTCAGCGACTTCGGTTGCTATCTACCGTTATTGCAAGAAAAGGGC  240

Qy     241 TATCAGCCTGATAATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC  300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TATCAGCCTGATAATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC  300

Qy     301 GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGCTAAGCGTGGAGCCTATATGGAA  360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGCTAAGCGTGGAGCCTATATGGAA  360

Qy     361 GAAGCGGCTCCTGCTGCAAATCGAAAAGCTTCGGCAAGCTTCGAGGTTACTCCAGCCAACTATAAC  420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAAGCGGCTCCTGCTGCAAATCGAAAAGCTTCGGCAAGCTTCGAGGTTACTCCAGCCAACTATAAC  420

Qy     421 ATTGAGAAGCCTGCTGCAAAAGCTTCGAGGTTACTCCAGCCAACTATAAC  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ATTGAGAAGCCTGCTGCAAAAGCTTCGAGGTTACTCCAGCCAACTATAAC  480

Qy     481 ACAACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard

; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9482
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(921)
US-10-072-851-9482

Query Match   99.0%; Score 911.4; DB 39; Length 921;
Best Local Similarity 99.3%; Pred. No. 2.2e-268;
Matches 915; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG  60

Qy    61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTA 120

Qy   121 GGTTATGATTACGTTATCTCATCGATACGGAAGAGACAAACTCAATCAGACCCGCTAT   180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGTTATGATTGCGTTATCTCATCGATACGGAAGAGACAAACTCAATCAGACCCGCTAT   180

Qy   181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTATTGCAAGAAAAGGGC  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTATTGCAAGAAAAGGGC  240

Qy   241 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300

Qy   301 GGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA  360

Qy   361 GAAGCGGCTCCTGCGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAAGCGGCTCCTGCGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC  420

Qy   421 ATTGAAGAAGCCTTCAAAAAGCTTCTGCTGGAGAAGTGGTTGCAGTGATCGAGCGGTTGAACTT 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATTGAAGAAGCCTTCAAAAAGCTTCTGCTGGAGAAGTGGTTGCAGTGATCGAGCGGTTGAACTT 480

Qy   481 ACACCTGCACAAATCGTCATTGCTGGAGAAGCTTCAGCCAACTATAAC             540
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ACACCTGCACAAATCGTCATTGCTGGAGAAGCTTCAGCCAACTATAAC             540

Qy   541 TTGCAAGAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCTTTCACACC 600
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Query Match   99.0%; Score 911.4; DB 31; Length 921;
Best Local Similarity 99.3%; Pred. No. 2.2e-268;
Matches 915; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy     1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG  60
Db     1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG  60
Qy    61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
Db    61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
Qy   121 GGTTATGATTACGTTATCTCATCGATACGGAAGAGACAAACTCAATCAGACCCGCTAT   180
Db   121 GGTTATGATTGCGTTATCTCATCGATACGGAAGAGACAAACTCAATCAGACCCGCTAT   180
Qy   181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTATTGCAAGAAAAGGGC  240
Db   181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTATTGCAAGAAAAGGGC  240
Qy   241 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
Db   241 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
Qy   301 GGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA  360
Db   301 GGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA  360
Qy   361 GAAGCGGCTCCTGCGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC  420
Db   361 GAAGCGGCTCCTGCGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC  420
Qy   421 ATTGAAGAAGCCTTCAAAAAGCTTCTGAACTTGGAGTTGTTACTCCAGCCAACTATAAC 480
Db   421 ATTGAAGAAGCCTTCAAAAAGCTTCTGAACTTGGAGTTGTTACTCCAGCCAACTATAAC 480
Qy   481 ACACCTGCACAAATCGTCATTGCTGGAGAAGCTTGATCGAGCGGTTGAACTT         540
Db   481 ACACCTGCACAAATCGTCATTGCTGGAGAAGCTTGATCGAGCGGTTGAACTT         540
Qy   541 TTGCAAGAAGCAGGTGCCAAACGCTTAGTGTCAGGTGTTGCAGGTGTCAGGTCCTTTCACACC 600
Qy   601 GCTCTCCCTTGAGCGCTGCTGCCAGAAAACTAGCTCAGCTGAAAACTAGCTCAGCTCAGAAAACTCCAGCGTAAGGTCAGT 660
Qy   661 GATTTTACTTGTCCCCTAGTCGGCAATACAGAGAAGCTGCTGTGATGCAATAACAGAGGAGACATT 720
Qy   721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCATGAAAGTATTGGGGTC 780
Qy   781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGAATTGATCAAACTTAATCGAGATTGGAAGAAAATAGTTTTGTCAGGT 840
Qy   841 TTTGTTAAAAAATTGATCAAAATCGCTCACTTAGCTCACTTAGCTCACTTAGCTGGAAGATCAAGCGAGTTTA 900
Qy   901 GTAGCACTTTTAGAAAAATAG 921
Db   901 GTAGCACTTTTAGAAAAATAG 921
```

RESULT 10
US-10-072-851-9482
; Sequence 9482, Application US/10072851
; GENERAL INFORMATION:

```
;    TOPOLOGY: linear
;    MOLECULE TYPE: DNA (genomic)
;    HYPOTHETICAL: NO
;    ANTI-SENSE: NO
PCT-US97-22578-43

Query Match           99.0%;   Score 911.4;   DB 1;   Length 3580;
Best Local Similarity 99.3%;   Pred. No. 4.1e-268;
Matches  915;  Conservative  0;  Mismatches  6;  Indels  0;  Gaps  0;

Qy     1 ATGACTAAAACAGCCTTTTTATTTGCTGCTCAAGGTGCCCAGTATCTAGGGATGGACGG  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   718 ATGACTAAAACAGCCTTTTTATTTGCTGCTCAAGGTGCCCAGTATCTAGGGATGGACGG 777

Qy    61 GATTTCTATCAGTATCCGATTGTCAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
         |||||||||| ||||||| |||||| |||||||||||||||| |||||||||||| ||
Db   778 GATTTCTATGATCAGTATCGATTGTTAAAGAAACGATTGATCGGCGAGTCAGGTGCTA 837

Qy   121 GGTTATGATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   838 GGTTATGATTTACTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 897

Qy   181 ACGCAACCAGCCATTCTAGCGACTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   898 ACGCAACCAGCCATTCTAGCGACTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC 957

Qy   241 TATCAGCCTGATATGGTTGCTCGTGGTTTGTGGTTTGTCTTCTTGGAGAATACTCTGCCTGGTGCCAAGC 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   958 TATCAGCCTGATATGGTTGCTCGTGGTTTGTGGTTTGTCTTCTTGGAGAATACTCTGCCTGGTGCCAAGC 1017

Qy   301 GGCGCCTTGACGTTTGAAGATGCGGTTGCCTTGCCTTGGTGTTGGTAGCTTAAGGCTGGAGCCTATATGGAA 360
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1018 GGCGCCTTGACGTTTGAAGATGCGGTTGCCTTGCCTTGGTGTTGGTAGCTTAAGGCTGGAGCCTATATGGAA 1077

Qy   361 GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGGCCAGTAGAGGTC 420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1078 GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGGCCAGTAGAGGTC 1137

Qy   421 ATTGAAGAAGCCTGTCAAAAAGTCTTCTGAACTTGGAGTTGGTTACTCCAGCCAACTATAAC 480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1138 ATTGAAGAAGCCTGTCAAAAAGTCTTCTGAACTTGGAGTTGGTTACTCCAGCCAACTATAAC 1197

Qy   481 ACACCTGCACAAATCGTCATTGCTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGGGGTTGAACTT 540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1198 ACACCTGCACAAATCGTCATTGCTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGGGGTTGAACTT 1257

Qy   541 TTGCAAGAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCCTTCACACC 600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1258 TTGCAAGAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCCTTCACACC 1317

Qy   601 GCTCTCCTTGAGCCTGCTAGCCAGAAACTCAGTGCTGAAACTCAGCTCAGGTAAGTTTTTCA 660
         |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1318 TCTCTCCTTGAACCTGCTAGCCAGAAACTCAGTGCTGAAACTCAGCTCAGGTAAGTTTTTCA 1377

Qy   661 GATTTTACTTGTCCCCCAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGAGGACATT 720
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1378 GATTTTACTTGTCCCCCAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGAGACATT 1437

Qy   721 GCTCAGCTCTTGACGCGTCAGGTCAGGTGAACCCGTTCGTTCTTATGAAGTATTGGGGTC 780
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1438 GCTCAGCTCTTGACGCGTCAGGTCAGGTGAACCCGTTCGTTCTTATGAAGTATTGGGGTC 1497

Qy   781 ATGCAAGAAGCAGGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGAAAGTCTTGTCAGGT 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1498 ATGCAAGAAGCAGGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGAAAGTCTTGTCAGGT 1557

Qy   841 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGGCGAGTTTA 900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1558 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGGCGAGTTTA 1617

Qy   901 GTAGCACTTTTAGAAAAATAG 921
         |||||||||||||||||||||
Db  1618 GTAGCACTTTTAGAAAAATAG 1638
```

RESULT 11
PCT-US97-22578-43
; Sequence 43, Application PC/TUS9722578
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Burgett, Stanley G.
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Jaskunas Jr., Stanley R.
; APPLICANT: Mills, Bradley J.
; APPLICANT: Norris, Franklin H.
; APPLICANT: Peery, Robert B.
; APPLICANT: Rosteck Jr., Paul R.
; APPLICANT: Skatrud, Paul L.
; APPLICANT: Smith, Michele C.
; APPLICANT: Rockey, Pamela K.
; APPLICANT: Young-Bellido, Michele
; TITLE OF INVENTION: Streptococcus Pneumoniae DNA Sequences
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Eli Lilly and Company
;   STREET: Lilly Corporate Center
;   CITY: Indianapolis
;   STATE: Indiana
;   COUNTRY: U.S.
;   ZIP: 46285
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US97/22578
;   FILING DATE:
;   CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Webster, Thomas D.
;   REGISTRATION NUMBER: 39,872
;   REFERENCE/DOCKET NUMBER: X-11162
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3580 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single

```
Qy    301  GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGGTGGAGCCTATATGGAA  360
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1534  GGGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGGTGGAGCCTATATGGAA 1593

Qy    361  GAAGCGGCCTCCTGCTCGACTCGGCAAGATGGTAGCAGTTCCAATACGCCAGTAGAGGTC  420
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1594  GAAGCGGCCTCCTGCTCGACTCGGCAAGATGGTAGCAGTTCCAATACGCCAGTAGAGGTC 1653

Qy    421  ATTGAAGAGCCTGTCAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC  480
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1654  ATTGAAGAGCCTGTCAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 1713

Qy    481  ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1714  ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT 1773

Qy    541  TTGCAAGAGCAGGTGCCAAACGCTGATTCCTCTTAAGGTGTCAGTCCCTTCACC  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1774  TTGCAAGAGCAGGTGCCAAACGCTGATTCCTCTTAAGGTGTCAGTCCCTTCACC 1833

Qy    601  GCTCTCCTTGAGCCTGCTAGCCAGAAACTAGCTGAAACTCAGCTCAGGTAAGTTTTTCA  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1834  GCTCTCCTTGAGCCTGCTAGCCAGAAACTAGCTGAAACTCAGCTCAGGTAAGTTTTTCA 1893

Qy    661  GATTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1894  GATTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT 1953

Qy    721  GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTCTCATGAAAGTATTGGGGTC  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1954  GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTCTCATGAAAGTATTGGGGTC 2013

Qy    781  ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAGTCTTGTCAGGT  840
           || |||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db   2014  ATCGAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAGTTTTGTCAGGT 2073

Qy    841  TTTGTTAAAAATTGATCAAACTGCTCACTTAGCTCATGTGAAGATCAAGCGAGTTTA  900
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2074  TTTGTTAAAAATTGATCAAACTGCTCACTTAGCTCATGTGAAGATCAAGCGAGTTTA 2133

Qy    901  GTAGCACTTTTAGAAAAATAG  921
           |||||||||||||||||||||
Db   2134  GTAGCACTTTTAGAAAAATAG 2154
```

RESULT 13
US-09-752-069A-256
; Sequence 256, Application US/09752069A
; GENERAL INFORMATION:
;...APPLICANT: Dougherty, Thomas J.
;...APPLICANT: Pucci, Michael J.
;...APPLICANT: Dougherty, Brian A.
;...APPLICANT: Davison, Daniel B.
;...APPLICANT: Bruccoleri, Robert E.
;...APPLICANT: Thanassi, Jane A.
;...APPLICANT: Farmer II, Bennett T.
;...TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
;...TITLE OF INVENTION: FOR CELL VIABILITY AND THEIR USES
;...FILE REFERENCE: D0001NP
;...CURRENT APPLICATION NUMBER: US/09/752,069A
;...CURRENT FILING DATE: 2000-12-29
;...PRIOR APPLICATION NUMBER: 60/174,089
;...PRIOR FILING DATE: 1999-12-30
;...NUMBER OF SEQ ID NOS: 338
;...SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 256
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-752-069A-256

Query Match   98.6%; Score 908.4; DB 29; Length 945;
Best Local Similarity 99.3%; Pred. No. 1.8e-267;

RESULT 12
US-60-068-175-555
; Sequence 555, Application US/60068175
; GENERAL INFORMATION:
;...APPLICANT: Lagace, Robert E.
;...APPLICANT: Corley, Neil C.
;...APPLICANT: Russo, Frank D.
;...APPLICANT: Hann, Amy L.
;...APPLICANT: Heath, Joe D.
;...APPLICANT: Finney, Gregory L.
;...TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
;...TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
;...NUMBER OF SEQUENCES: 1175
;...CORRESPONDENCE ADDRESS:
;...ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;...STREET: 3174 PORTER DRIVE
;...CITY: PALO ALTO
;...STATE: CALIFORNIA
;...COUNTRY: USA
;...ZIP: 94304
;...COMPUTER READABLE FORM:
;...MEDIUM TYPE: Floppy disk
;...COMPUTER: IBM PC compatible
;...OPERATING SYSTEM: PC-DOS/MS-DOS
;...SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;...CURRENT APPLICATION DATA:
;...APPLICATION NUMBER: US/60/068,175
;...FILING DATE: HEREWITH
;...CLASSIFICATION:
;...ATTORNEY/AGENT INFORMATION:
;...NAME: CERRONE, MICHAEL C.
;...REGISTRATION NUMBER: 39,132
;...REFERENCE/DOCKET NUMBER: PM-0009-2 P
;...TELECOMMUNICATION INFORMATION:
;...TELEPHONE: (650) 855-0555
;...TELEFAX: (650) 845-416
; INFORMATION FOR SEQ ID NO: 555:
;...SEQUENCE CHARACTERISTICS:
;...LENGTH: 9753 base pairs
;...TYPE: nucleic acid
;...STRANDEDNESS: double
;...TOPOLOGY: circular
;...MOLECULE TYPE: genomic DNA
;...IMMEDIATE SOURCE:
;...CLONE: SPN2c557
US-60-068-175-555

Query Match   99.0%; Score 911.4; DB 50; Length 9753;
Best Local Similarity 99.3%; Pred. No. 6.5e-268;
Matches 915; Conservative 0; Mismatches 0; Indels 6; Gaps 0;

```
Qy      1  ATGACTAAAACAGCCTTTTTATTTGCTGACGTGCCAGGTATCTAGGGATGGGACGG   60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234  ATGACTAAAACAGCCTTTTTATTTGCTGACGTGCCAGGTATCTAGGGATGGGACGG 1293

Qy     61  GATTTCTATGATCAGTAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTGCTC  120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db   1294  GATTTCTATGATCAGTAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTGCTA 1353

Qy    121  GGTTATGATTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1354  GGTTATGATTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 1413

Qy    181  ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTCGAAGAAAGGGC  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1414  ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTCGAAGAAAGGGC 1473

Qy    241  TATCAGCCTGATATGGTTGCTCGGTTTGTCTTCTTGGAGAATACTCTGCCTTGGTGGCAAGC  300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1474  TATCAGCCTGATATGGTTGCTCGGTTTGTCTTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 1533
```

APPLICANT: RUSSO, FRANK D.
APPLICANT: HANN, AMY L.
APPLICANT: HEATH, JOE D.
APPLICANT: FINNEY, GREGORY L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/60/061,998
 FILING DATE:
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
 NAME: CERRONE, MICHAEL C.
 REGISTRATION NUMBER: 39,132
 REFERENCE/DOCKET NUMBER: PM-0006-2P
TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 494:
SEQUENCE CHARACTERISTICS:
 LENGTH: 5963 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 IMMEDIATE SOURCE:
 CLONE: SPN1c499
US-60-061-998-494

Query Match   96.8%;   Score 891.6; DB 50;   Length 5963;
Best Local Similarity   98.9%;   Pred. No. 6.2e-262;
Matches 908; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

Qy   1 ATGACTAAAACAGCCTTTTATTTGCTGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2919 ATGACTAAAACAGCCTTTTATTTGCTGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 2978

Qy   61 GATTTCTATGATCAGTATCCGATTGTCAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   2979 GATTTCTATGATCAGTATCCGATTGTTAAAGAAACGATTGATCGAGCGAGTCAGGTGCTA 3038

Qy   121 GGTTATGATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3039 GGTTATGATTTGCGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 3098

Qy   181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCGTTATTGCAAGAAAGGGC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3099 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCGTTATTGCAAGAAAGGGC 3158

Qy   241 TATCAGCCTGATATGGTTGCTCGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3159 TATCAGCCTGATATGGTTGCTCGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 3218

Qy   301 GGCGCCTTGGATTTGAAGATGCGGTTGCAAGATGGTAGCAGTTCCAATACGCCAGTAGGAA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3219 GGCGCCTTGGATTTGAAGATGCGGTTGCAAGATGGTAGCAGTTCCAATACGCCAGTAGGAA 3278

Qy   361 GAAGCGGCTCCTGCACTCTGGCAAGATGGTAGCAGTTCCAATACGCCAGTAGAGGTC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3279 GAAGCGGCTCCTGCACTCTGGCAAGATGGTAGCAGTTCCAATACGCCAGTAGAGGTC 3338

Matches 912; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy   1 ATGACTAAAACAGCCTTTTATTTGCTGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGACTAAAACAGCCTTTTATTTGCTGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60

Qy   61 GATTTCTATGATCAGTATCCGATTGTCAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   61 GATTTCTATGATCAGTATCCGATTGTTAAAGAAACGATTGATCGAGCGAGTCAGGTGCTA 120

Qy   121 GGTTATGATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGTTATGATTTGCGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 180

Qy   181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCGTTATTGCAAGAAAGGGC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCGTTATTGCAAGAAAGGGC 240

Qy   241 TATCAGCCTGATATGGTTGCTCGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TATCAGCCTGATATGGTTGCTCGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 300

Qy   301 GGGCCCTTGGATTTGAAGATGCGGTTGCCTGCGACTCTGGTAGCTAAGCGTGAGCCTATATGGAA 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGGCCCTTGGATTTGAAGATGCGGTTGCCTGCGACTCTGGTAGCTAAGCGTGAGCCTATATGGAA 360

Qy   361 GAAGCGGCTCCTGCTCCTGCGACTCTGGTAGCAGTTCCAATACGCCAGTAGAGGTC 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAAGCGGCTCCTGCTCCTGCGACTCTGGTAGCAGTTCCAATACGCCAGTAGAGGTC 420

Qy   421 ATTGAAGAGAGCCTGTCAAAAAGCTTCTGAACTTGGAGTTGGTTACTCCAGCCAACTATAAC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATTGAAGAGAGCCTGTCAAAAAGCTTCTGAACTTGGAGTTGGTTACTCCAGCCAACTATAAC 480

Qy   481 ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTGATCGAGCGGTTGAACTT 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTGATCGAGCGGTTGAACTT 540

Qy   541 TTGCAAGAAGCAGTGCCAAACGTTGATTCCCTTAAGGTGTCAGGTGTCAGGTCCCTTCACACC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TTGCAAGAAGCAGTGCCAAACGTTGATTCCCTTAAGGTGTCAGGTGTCAGGTCCCTTCACACC 600

Qy   601 GCTCTCCTTGAGCCTGCTAGCCAGCAGAAACTAGCTGAAACTCAGGTAAGTTTTTCA 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCTCTCCTTGAAACTGCTAGCCAGCAGAAACTAGCTGAAACTCTGGCTAGCTAAGTTTTTCA 660

Qy   661 GATTTTACTTGTCCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAAAAAGAGGACATT 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GATTTTACTTGTCCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAAAAAGAGGACATT 720

Qy   721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCATGAAAGTATTGGGGTC 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCATGAAAGTATTGGGGTC 780

Qy   781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGGAGATTGGACCGGGGAAAGTCTTGTCAGGT 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGGAGATTGGACCGGGGAAAGTCTTGTCAGGT 840

Qy   841 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA 900

Qy   901 GTAGCACTTTAGAAAAA 918
             |||||||||||||||||
Db   901 GTAGCACTTTAGAAAAA 918

RESULT 14
US-60-061-998-494
; Sequence 494, Application US/6006199B
GENERAL INFORMATION:
 APPLICANT: LAGACE, ROBERT E.
 APPLICANT: CORLEY, NEIL C.

Qy   421 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3339 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 3398

Qy   481 ACACCT-GCACAAATCGTCATTGCTCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACT 539
          ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3399 ACACCTGGCACAAATCGTCATTGCTCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACT 3458

Qy   540 TTTGCAAGAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCCTTTCACAC 599
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3459 TTTGCAAGAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCCTTTCACAC 3518

Qy   600 CGCTCTCCTTGAGCCTGCTAGCCAGAAACTAGCTGAAACTTCAGCTCAGGTAAGTTTTTC 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3519 CTCTCTCCTTGAACCTGCTAGCCAGAAACTAGCTGAAACTTCGGCTCAGGTAAGTTTTTC 3578

Qy   660 AGATTTTACTTGTCCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACAT 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3579 AGATTTTACTTGTCCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACAT 3638

Qy   720 TGCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGT 779
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3639 TGCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGT 3698

Qy   780 CATGCAAGAGCAGGCATAAGCAACTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGG 839
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3699 CATGCAAGAGCAGGCATAAGCAACTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGG 3758

Qy   840 TTTTGTTAAAAAAATTGATCAAAACTGCTCACTTAGCTCACTAGCTCATGTGGAAGATCAAGCGGAGTTT 899
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3759 TTTTGTTAAAAAAATTGATCAAAACTGCTCACTTAGCTCACTAGCTCATGTGGAAGATCAAGCGGAGTTT 3818

Qy   900 AGTAGCACTTTTAGAAAA 917
          ||||||||||||||||
Db   3819 AGTAGCACTTTTAGAAAA 3836

AATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTTTTGCAAGAAGC 551
AATCGTCATTGC-TGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTTTTTGCAAGAAGC 180

Qy   492 AATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTTTTGCAAGAAGC 551
          ||||||||||| ||||||||||||||||||||||||||||||||||||||| ||||||||
Db   121 AATCGTCATTGC-TGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTTTTTGCAAGAAGC 180

Qy   552 AGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCCTTTCACACCGCTCTCCTTGA 611
          ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   181 AGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCCTTTCACACCGCTCTCCTTGA 240

Qy   612 GCCTGCTAGCCAGAAACTAGCTGAAACTTCAGCTCAGGTAAGTTTTTCAGATTTTTACTTG 671
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GCCTGCTAGCCAGAAACTAGCTGAAACTTCAGCTCAGGTAAGTTTTTCAGATTTTTACTTG 300

Qy   672 TCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAAAAAGAGAGACATTGCTCAGCTCTT 731
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAAAAAGAGAGACATTGCTCAGCTCTT 360

Qy   732 GACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTCATGCAAGAAGC 791
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTCATGCAAGAAGC 420

Qy   792 AGGCATAAGCAACTTATCGAGATTGGACGGGGAAAGTCTTGTCAGGTTTTGTTAAAAA 851
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 AGGCATAAGCAACTTATCGAGATTGGACGGGGAAAGTCTTGTCAGGTTTTGTTAAAAA 480

Qy   852 AATTGATCAAAACTGCTCACTTAGCTCACTAGCTCATGTGGAAGATCAAGCGGAGTTTAGTAGCACTTTT 911
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 AATTGATCAAAACTGCTCACTTAGCTCACTAGCTCATGTGGAAGATCAAGCGGAGTTTAGTAGCACTTTT 540

Qy   912 AGAAAAA 918
          |||||||
Db   541 AGAAAAA 547

Search completed: June 11, 2003, 19:45:30
Job time : 2192 secs

RESULT 15
US-09-308-397-5
; Sequence 5, Application US/09308397
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel R.
; APPLICANT: Lonsdale, John T.
; APPLICANT: Payne, David J.
; APPLICANT: Pearson, Stewart C.
; APPLICANT: Van Aller, Glenn
; TITLE OF INVENTION: Novel FabD
; FILE REFERENCE: P50593
; CURRENT APPLICATION NUMBER: US/09/308,397
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: US 60/031,160
; EARLIER FILING DATE: 1996-11-18
; EARLIER APPLICATION NUMBER: PCT/US97/20992
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-308-397-5

Query Match   57.5%; Score 529.4; DB 17; Length 547;
Best Local Similarity 98.0%; Pred. No. 3.8e-151;
Matches 536; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy   372 TGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTCATTGAAGAAGC 431
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 TGCTGAACTTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTCATTGAAGAAGC 60

Qy   432 CTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAACACCTGCACA 491
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAACACCTGCACA 120

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                    Copyright   GenCore version 5.1.6
                    Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          June 11, 2003, 18:04:17 ; Search time 695 Seconds
                                            (without alignments)
                                            8797.240 Million cell updates/sec

Title:           US-09-308-397-1
Perfect score:   921
Sequence:        1 atgactaaacagcctttt........tagcactttagaaaatag 921

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        760234 seqs, 319262570 residues

Total number of hits satisfying chosen parameters:   15204468

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_NA_New:*
                 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
                 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
                 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
                 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
                 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
                 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2:*
                 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3:*
                 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
                 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
                10: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
                11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	911.4	99.0	921	9	US-10-282-122A-37621	Sequence 37621, A
2	459.4	49.9	918	9	US-10-282-122A-36004	Sequence 36004, A
3	439.4	47.7	939	9	US-10-282-122A-38525	Sequence 38525, A
4	388.8	42.2	927	8	US-10-369-493-42057	Sequence 42057, A
5	350.8	38.1	927	9	US-10-282-122A-20712	Sequence 20712, A
6	350.8	38.1	948	6	US-09-134-000C-1582	Sequence 1582, Ap
7	350.8	38.1	948	6	US-09-134-000C-1582	Sequence 1582, Ap
8	350.8	38.1	948	9	US-10-434-665-1582	Sequence 1582, Ap
9	316.8	34.4	915	9	US-10-282-122A-21491	Sequence 21491, A
10	315.2	34.2	987	8	US-10-417-884-3319	Sequence 3319, Ap
11	217.6	23.6	939	9	US-10-282-122A-41191	Sequence 41191, A
12	196.4	21.3	930	9	US-10-282-122A-32186	Sequence 32186, A
13	196.4	21.3	939	9	US-10-282-122A-21907	Sequence 21907, A
14	196.4	21.3	1830121	4	US-08-487-429B-1	Sequence 1, Appli
15	196.4	21.3	1830121	9	US-10-329-960-1	Sequence 1, Appli
16	189.8	20.6	2810	10	US-60-453-134-364	Sequence 364, App
17	185.6	20.2	930	8	US-10-369-493-24480	Sequence 24480, A
18	185.6	20.2	930	9	US-10-282-122A-20335	Sequence 20335, A
19	179.6	19.5	954	8	US-10-369-493-46809	Sequence 46809, A
20	179.4	19.5	939	9	US-10-282-122A-31257	Sequence 31257, A
21	178.4	19.4	927	9	US-10-282-122A-15949	Sequence 15949, A
22	177.8	19.3	954	9	US-10-282-122A-16221	Sequence 16221, A
23	168	18.2	930	9	US-10-282-122A-38967	Sequence 38967, A
24	166.8	18.1	942	8	US-10-369-493-41012	Sequence 41012, Ap
25	165.6	18.0	2301	8	US-10-398-221-3519	Sequence 3519, Ap
26	165	17.9	930	9	US-10-282-122A-42230	Sequence 42230, A
27	164.8	17.9	930	8	US-10-282-122A-39704	Sequence 39704, A
28	164.8	17.9	9686	8	US-10-194-163A-1003	Sequence 1003, Ap
29	164.8	17.9	9686	8	US-10-194-163-1003	Sequence 1003, Ap
30	162.4	17.6	319630	8	US-10-398-221-7	Sequence 7, Appli
31	162.4	17.6	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
32	160.4	17.4	942	9	US-10-282-122A-24478	Sequence 24478, A
33	158.8	17.2	926	9	US-10-282-122A-23167	Sequence 23167, A
34	157	17.0	1092	9	US-10-282-122A-31669	Sequence 31669, A
35	151.6	16.5	918	9	US-10-369-493-42861	Sequence 42861, A
36	149.2	16.2	930	9	US-10-282-122A-36638	Sequence 36638, A
37	142.4	15.5	948	9	US-10-282-122A-17057	Sequence 17057, A
38	140	15.2	945	9	US-10-282-122A-25339	Sequence 25339, A
39	139.2	15.1	843	8	US-10-369-493-33918	Sequence 33918, A
40	137.6	14.9	771	9	US-10-446-203-272	Sequence 272, App
41	136.6	14.8	2272325	9	US-10-018-470-1	Sequence 1, Appli
42	136.6	14.8	2272325	9	US-10-018-470A-1	Sequence 1, Appli
43	134.4	14.6	885	9	US-10-282-122A-12672	Sequence 12672, A
44	133.8	14.5	942	9	US-10-282-122A-9898	Sequence 9898, Ap
45	133.4	14.5	927	9	US-10-282-122A-29553	Sequence 29553, A

ALIGNMENTS

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RESULT 1
US-10-282-122A-37621
; Sequence 37621, Application US/10282122A
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT: Zamudio, Carlos
;  APPLICANT: Malone, Cheryl
;  APPLICANT: Haselbeck, Robert
;  APPLICANT: Ohlsen, Kari
;  APPLICANT: Zyskind, Judith
;  APPLICANT: Wall, Daniel
;  APPLICANT: Trawick, John
;  APPLICANT: Carr, Grant
;  APPLICANT: Yamamoto, Robert
;  APPLICANT: Forsyth, R.
;  APPLICANT: Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA_034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37621
; LENGTH: 921
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; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-282-122A-37621

Query Match   99.0%;   Score 911.4;   DB 9;   Length 921;
Best Local Similarity 99.3%;   Pred. No. 6e-270;
Matches   915; Conservative   0;   Mismatches   6;   Indels   0;   Gaps   0;

Qy   1 ATGACTAAAACAGCCTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 ATGACTAAAACAGCCTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 60

Qy   61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGTGCTC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGTGCTA 120

Qy   121 GGTTATGATTTACGTTATCTCATCGATGAAGGAAGACAAACTCAATCAGACCCGCTAT 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGTTATGATTTGCGTTATCTCATCGATGAAGGAAGACAAACTCAATCAGACCCGCTAT 180

Qy   181 ACGCAACCAGCCATTCGGACTCGGTGCTATCTACCGTTTATTGCAAGAAAAGGGC 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ACGCAACCAGCCATTCGGACTCGGTGCTATCTACCGTTTATTGCAAGAAAAGGGC 240

Qy   241 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGCAAGC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGCAAGC 300

Qy   301 GGCGCCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGCGCCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCGGTGGAGCCTATATGGAA 360

Qy   361 GAAGCCGGCTCCTGCTGACTCTCGGCCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGTC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GAAGCCGGCTCCTGCTGACTCTCGGCCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGTC 420

Qy   421 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 480

Qy   481 ACACCTGCACAAATCGTCATTGCTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT 540
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ACACCTGCACAAATCGTCATTGCTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT 540

Qy   541 TTGCAAGAAGCAGGTGCCAAACGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCCTTTCACACC 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 TTGCAAGAAGCAGGTGCCAAACGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCCTTTCACACC 600

Qy   601 GCTCTCCTTGAGCCTGCTAGCCAGGAAACTCTAGCTGAAACTCTGAAACTCTGGCCTCAGGTAAGTTTTCA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 TCTCTCCTTGAACCTGCTAGCCAGGAAACTCTAGCTGAAACTCTGGCCTCAGGTAAGTTTTTCA 660

Qy   661 GATTTTACTTGTCCCCTAGTCGGCAATACAGAGAGCTGCTGTGAATGCAAAAGAGAGACATT 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 GATTTTACTTGTCCCCTAGTCGGCAATACAGAGAGCTGCTGTGAATGCAAAAGAGAGACATT 720

Qy   721 GCTCAGTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721 GCTCAGTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC 780

Qy   781 ATGCAAGAAGCAGGCATAAGCAATAAGCACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781 ATGCAAGAAGCAGGCATAAGCAATAAGCACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT 840

Qy   841 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGGAAGATCAAGCGAGTTTA 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGGAAGATCAAGCGAGTTTA 900

Qy   901 GTAGCACTTTAGAAAAATAG 921
           ||||||||||||||||||||
Db   901 GTAGCACTTTAGAAAAATAG 921

RESULT 2
US-10-282-122A-36004
; Sequence 36004, Application US/10282122A
; GENERAL INFORMATION:
;   APPLICANT: Wang, Liangsu
;   APPLICANT: Zamudio, Carlos
;   APPLICANT: Malone, Cheryl
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Kari
;   APPLICANT: Zyskind, Judith
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John
;   APPLICANT: Carr, Grant
;   APPLICANT: Yamamoto, Robert
;   APPLICANT: Forsyth, R.
;   APPLICANT: Xu, H.
;   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;   FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36004
;   LENGTH: 918
;   TYPE: DNA
;   ORGANISM: Streptococcus mutans
US-10-282-122A-36004

Query Match   49.9%;   Score 459.4;   DB 9;   Length 918;
Best Local Similarity 68.8%;   Pred. No. 1.3e-130;
Matches   631; Conservative   0;   Mismatches 286;   Indels   0;   Gaps   0;

Qy   1 ATGACTAAAACAGCCTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 60
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Db   1 ATGACAAAAACACAGCATTTTTATTTGCTGGCCAAGAGCTCAAAAACTTGGTATGGGATGGCAAGT 60

Qy   61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGTGCTC 120
           |||| ||||||||||| |||| ||||||||||||||||||
Db   61 GATTTGTATGAAATTACCCAGTTGTCAAAGAGACTTTTAAAACCGCTCAATTCAATTTG 120

Qy   121 GGTTATGATTTACGTTATCTCATCGATGAAGGAAGACAAACTCAATCAGACCCGCTAT 180
           ||||| || |||||| |||| |||||| ||||||| ||||| |||| |||||
Db   121 GGATATGATGTTGCGTGTCGTTTGATTGATGAATGAATGATGAAGAAATCAAACACGTTAT 180

Qy   181 ACGCAACCAGCCATTCGGACTCGGTGCTATCTACCGTTTATTGCAAGAAAAGGGC 240
           ||||||||||| |||| ||||||| ||||| ||||| |||||| |||| ||||
Db   181 ACGGCAGCCGGCGATTTTTAACAACTTCAGTAGCTAATTTATGTCTTTTTGAAAAAGT 240

Qy   241 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGCAAGC 300
           |||| || |||| ||| ||| |||| |||| || |||| ||| ||||||| |||||
Db   241 TATCAACCGACATTGTTGCTGACTGTCACTAGGAGAATACTCTGCCTCGCTTGTTGTTGCGCC 300

Qy   901 GTAGCACTTTAGAAAAATAG 921

Db   901

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RESULT 3
US-10-282-122A-38525
; Sequence 38525, Application US/10282122A
; GENERAL INFORMATION:
;   APPLICANT: Wang, Liangsu
;   APPLICANT: Zamudio, Carlos
;   APPLICANT: Malone, Cheryl
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Karl
;   APPLICANT: Zyskind, Judith
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John
;   APPLICANT: Carr, Grant
;   APPLICANT: Yamamoto, Robert
;   APPLICANT: Forsyth, R.
;   APPLICANT: Xu, H.
;   TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;   FILE REFERENCE: ELITRA.034A
;   CURRENT APPLICATION NUMBER: US/10/282,122A
;   CURRENT FILING DATE: 2003-02-20
;   PRIOR APPLICATION NUMBER: 60/191,078
;   PRIOR FILING DATE: 2000-03-21
;   PRIOR APPLICATION NUMBER: 60/206,848
;   PRIOR FILING DATE: 2000-05-23
;   PRIOR APPLICATION NUMBER: 60/207,727
;   PRIOR FILING DATE: 2000-05-26
;   PRIOR APPLICATION NUMBER: 60/230,335
;   PRIOR FILING DATE: 2000-09-06
;   PRIOR APPLICATION NUMBER: 60/230,347
;   PRIOR FILING DATE: 2000-09-09
;   PRIOR APPLICATION NUMBER: 60/242,578
;   PRIOR FILING DATE: 2000-10-23
;   PRIOR APPLICATION NUMBER: 60/253,625
;   PRIOR FILING DATE: 2000-11-27
;   PRIOR APPLICATION NUMBER: 60/257,931
;   PRIOR FILING DATE: 2000-12-22
;   PRIOR APPLICATION NUMBER: 60/267,636
;   PRIOR FILING DATE: 2001-02-09
;   PRIOR APPLICATION NUMBER: 60/269,308
;   PRIOR FILING DATE: 2001-02-16
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 78614
;   SOFTWARE: Patentin version 3.1
; SEQ ID NO 38525
;   LENGTH: 939
;   TYPE: DNA
;   ORGANISM: Streptococcus pyogenes
US-10-282-122A-38525

  Query Match             47.7%;  Score 439.4;  DB 9;  Length 939;
  Best Local Similarity   67.3%;  Pred. No. 1.9e-124;
  Matches  620;  Conservative   0;  Mismatches  301;  Indels    0;  Gaps    0;

Qy          1 ATGGACTAAAACAGCCTTTATTTGCTGCCAAGGTGCCCAGTATCTAGGGATGGGACGG 60
              ||| || ||||||||| ||||||||||| || ||||||| | | ||||||||| | ||
Db          1 ATGACAAAGACAGCGCCTTTTATTTGCCGGTCAAGGTGCTCAAAAATTAGGGATGGCAAGG 60

Qy         61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGTGCTC 120
              ||||| ||||| | ||  |||| ||||| ||| |||  ||||||||| || |||  || |
Db         61 GATTTTTATGATAACTTTGCCATTGTAAAGAAAAAACCTTTGATCAAGCTAGTCAAGTATTG 120

Qy        121 GGTTATGATTACGTTATCTCATCGATACGGGAAGAAGACAAATCAATCAGACCCGCTAT 180
              |||||||||| |||  |  |  || || ||| |||||  |   ||| || ||  ||| ||
Db        121 GGATACGATTTGCGCGTTGACCTTGGTTGATTGATGATGATGACGAGTTAAAACTTAATCAAACTAGCTAT 180

Qy        181 ACGCAACAGCCATTCTAGCGACTTCGGTTGCTATCGTTGGTGGAGAAATACCTCGCGTTT 240
              ||| |||||||| ||| ||| ||  ||| |  ||  ||| ||||| ||||| | ||  | |
Db        181 ACGCAACAGCCATTTTGACATCATCAATTGCTATTTACCGTATTTACCGTGTTTACATCAC 240

Qy        241 TATCAGCTGATATGGTTGCTGGTGTTGTCTCTTGGGACGAAATACTCGCGTTGGTGCAAGC 300
              |||||||||| ||||  || | ||||| ||  |||| || ||||| || |||  ||  ||
Db        241 GTTAAACCGGATATGGTAGCTGGTCGTCTTCCTAGGAGAAATACTCAGCTTTGGTAGTAGCATCA 300

Qy        301 GGGCGCCTTGATTTGAAGATGCGGTTGCCTTGGTGAGCTAAGCCGTTATATGGAA 360
              || | | ||||||||||||| |  |||||||||||||| ||||| |  | |||||
Db        301 GGGCGCACTCTCTTCTTTTTGAAGATACCATCTTAGTAGCTAAGAGAGGCCGCTGATGGAG 360

Qy        361 GAAGCGGCTCCTGCGACTCTGGCAAGATGTAGCAGTTCTCAATACGCCAGTAGAGGTC 420
              ||||| ||| | |||  |  ||| ||||| |||||| || ||||| || || ||| |
Db        361 GAAGCAGCACCACAAGGATCGGAAAGAAGAAGATGGTTGCCGTTGCCGTTATGAATACAGAGACGTGCAAGTC 420

Qy        421 ATTGAAGAAGCCGTCAAAAAGTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC 480
              |||||||| || ||||||||||| ||| ||| ||||| |||| ||  | ||  ||||
Db        421 ATCGAAGAAGTCGTCAAAATAGTCGTCAAACTGGTCTTCCAGCAAACTATAAT 480

Qy        481 ACACCTGCACAAATCGTCATTGCTGCGGAGAAGTGGTTGCAGTAGCGCGGTTGAACTT 540
              || ||| | ||| || ||  ||||| | ||||| ||| | ||| | ||  |||||||
Db        481 ACTCCTAGTCAAATTGTTAATTGTGGTTGGTGGCTCAGACAGATCTGTGAACGTTGCAGTTGAACTT 540

Qy        541 TTGCAAGAAGCAGGTGCCAAACGTTGATTCCTCTTAAGTGTGTCAGTTCCCTTTCACACC 600
              ||| |  | | ||| |  || | ||||  ||| || |||| ||||| |||| || || | |
Db        541 TTAAAGGAAAAGGGGAGTTAAGCTGTTTAATCCCTTTAAACGTGTCAGTTCGTTAGTCAGTTTTCA 600

Qy        601 GCTCTCCTGAGCCTGCTAGCCAGAAACTAGCTGAAACTTCTAGCTCAGTAAGTTTTCA 660
              || | || |||   | ||||| |  | |||||| |  ||   |||| |||  ||| ||
Db        601 GCTTTGTGAGACCAGTAGCCGCAATACAGAGAGCGTCTGTGTTATTTGGCTTATGGCAGTTTTTA 660

Qy        661 GATTTTACTTGTCCCCTAGTCGGCAATACAAAGAGGACATT 720
              ||||| |  ||| | ||||||  | ||||| |||||| ||
Db        661 GACTTTCAAGATTCCTTTGGTTGGTAATACCCGAAGCTAATATTATGAAAAAGACCGTATC 720

Qy        721 GCTCAGCTCTTGAGCGTGCGGTTGCTGCGGAACCCGTTCGTTCTATGAAGTATTGGGGTC 780
Db        721 GCTTTGTTAGAACCAGCGCCGCTTGGTGATGAGTTGGCTAAAGATACAACTTCAGT 780

Qy        781 ATGGAAGAAGCAGGCAGGAGGCATAAGCAAACTTATCGAGATTGCGCCGGGGAAAGTCTTTGTCAGGT 840
Db        781 ATGAAGAAGCTGTCAATAGCTGCCAAGTGTCTCCAGCAAACTATAAT 840

Qy        841 TTTGTTAAAAAAATTGATCAAACTGCTCACTCATGTGGAAGATCAGGCCAGTTTA 900
Db        841 TTTGTGAAAAAGATTGATAAATCTGCAAGATCTGCCAAAATCTCCAGCTGTTGAAGAGACTTAGCTAGTAGTTTG 900

Qy        901 GTAGCACTTTTAGAAAA 917
Db        901 CAGGCTTTCTTAGATAA 917
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Qy 721 GCTCAGCTCTTGACGGCGGTCAGTCAAGGAACCCGTTCGTTCGTTTCTTATGAAAGTATTGGGGTC 780
         |||||||| ||||||||| |||| ||| | ||| | |||||||| ||||
Db 721 CCAGAACTATTAGCCCGTCAAGTCAAGTCATGGAGCCTGTTCGTTCGTTTTATGACAGTGTTGCGACT 780

Qy 781 ATGCAAGAAGCAGGCATAAACAACTTTATCGAGATTGACACGGGGAAAGTCTTGTCAGGT 840
         |||| | |||| | ||| || ||||||| |||
Db 781 TTAGTAGAAAGTGGCATAACACAATTCATTGAGGTAGGACCAGGTAAGGTTTTGACAGGT 840

Qy 841 TTTGTTAAAAAAATTGATAAAAAATTTACTATGTACTACTAGTGTTGAAAACATGGTAAGCTTA 900
         |||||||||||| |||| |||| || ||| | || |||||||||| |||
Db 841 TTTGTGAAGAAAATTGATAAAAAATTTACTATGTACTAGTGTTGAAACACATGGTAAGCTTA 900

Qy 901 GTAGCACTTTTAGAAAAATAG 921
         |||||| |||| |||
Db 901 CGTTTATTTTTTAGATAGAGAG 921

RESULT 4
US-10-369-493-42057
; Sequence 42057, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 42057
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Lactococcus lactis
US-10-369-493-42057

Query Match   42.2%; Score 388.8; DB 8; Length 927;
Best Local Similarity 64.6%; Pred. No. 7.3e-109;
Matches 598; Conservative 0; Mismatches 322; Indels 6; Gaps 1;

Qy   1 ATGACTAAAACAGCCTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 60
         ||||||||||| || ||| ||| ||||||| ||| | |||| |||||| |||
Db   1 ATGACTAAAACAGCATTTTATTCTCAGGTCAAGGCACAAAAAGCTTGGAATGCCACGT 60

Qy   61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACAGATTGATCGAGCGAGTCAGGTGCTC 120
         | | |||| |||| | |||| ||| |||||||| || |||||| | || |||
Db   61 GACTTATATGACCAATAGCAAATATGAAACAGACTTTGATGAAGCAACTTTTGATGAAGTCAAGCTTA 120

Qy 121 GGTTATGCATTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 180
         |||| || |||| | | ||| |||| |||||||||| | | ||||||| || | |||
Db 121 GGATATGCATTTGCAGCTTGATTGATTAATGATGAAGAAAACTAAATGAAACAAGTAC 180

Qy 181 ACGCAACCAGCCATTCTAGCGACTTCGGTGCTATCCGGTTATTGCAAGAAAAGGGC 240
         || | ||| || || | || || ||||| | || ||| |||||| |||||
Db 181 ACTCAACTGCAATTTTAACAACCTGTGCTGCTATTTTACCTTTGTTAAGTGAGAATGGG 240

Qy 241 TATCAGCCTGATATGGTTGCTGGTTTGTCTCCTGGAGAATACTCTGCCTTGGTGGCAAGC 300
         ||| || |||||| | || || ||| |||| ||| ||| | | || ||||| |||
Db 241 ATTAAACCTGACCTTGTTGCTGGTCTTAATGGTCGCTGTAAATGTGCTAGAATTTCTGCTTCA 300

Qy 301 GGCGCCTTGAAGATGCGGTTGCCTTGGTTAAGCGTGAGCCTATATGGAA 360
         ||| |||| || ||| | ||| || || | | ||||| |||| | |||
Db 301 GGAATCATTGATTTTCAAGAAGCAGTTAAGCTTAGCTTAGAGTAGCTAAACGTTGTCAATATATGACA 360

Qy 361 GAAGCGGCTCCTGCTAGCTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 420
         ||||| | || ||| || | ||| ||||| ||| | | || || ||| || ||
Db 361 GAAGCTGCACCGACTGGTTCTGCGTTCGTAAAATGGTCGCTGTAAATGAACAACAGACCAGCCTTG 420

Qy 421 ATTGAAGAAGCCTGTCGTCAAAAAGCTTCTGAACTT------GGAGTGGTTACTCCAGCCAAC 474

RESULT 5
US-10-282-122A-20712
; Sequence 20712, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636

Db 421 ATTGAAGAAATTTGCCAGAAGCGGCCCAATTTAAAGCGGAAGTGGTTATTGTGAGTCCAGCAAAT 480

Db 475 TATAACACCTGCACAAATCGTCATTGCTGGACGGGTGGTTGCAGTTGATCGAGCGGGTT 534

Db 481 TATAACACGCCCGCACAAATTGTTATTGGTGGTGGTTGAGGTCGGTTGATTATGCTGTT 540

Qy 535 GAACTTTGCAAGAGCAGGTGCCAAACGCTTGATCCTCCTTAAGGTGTCAGGTGTCCCTT 594
         ||||||||||||||||| ||||||||||| | |||| || |||
Db 541 GAGTTGCTAAAAGAGAAGCCGGAGTTCGTAAACTTATTGAATTAAAAGTTTCAGGACCTTTC 600

Qy 595 CACACCGCTCTCCTTGACCTGCTGAGCCTGTGAGCCAGAAACTAGCTGAAACTCAGGTAAGT 654
         |||||| ||| | ||| || || | || ||| || ||| |||| | | ||||
Db 601 CATCAGCAGTAATTTAAACCAGCATCTGAAAAAATTGGCTTTGGAGCTTGATAAAAATTGAT 660

Qy 655 TTTCAGATTTTACTTGTCCCCAGTCGGCAATACAGTCAAATCTCAAATACGAGTGCTAAAGTAATGGAAAATGAT 714
         ||||| | | ||| ||| |||| || | || | || ||||||| || | |||||
Db 661 TTTAGACCTTTTGAATTACCATTAATCTCAAATCAAATACGAGTGTTCGTTCTTCATGAAAGTATT 720

Qy 715 GACATTGCTCAGTCTTGCACGCGTCAGTTCAAGGAACCCGTTCGTTCGTTCTTCTATGAAAGATTCGGTT 774
         |||||||| | || | || ||| ||| | |||||| || ||| ||||||| |||||
Db 721 GAAGTCAAAGGACTTTTGACGCGTCAAGTCATGGAACCAGTTCGTTCGTTTTATGATCGGTT 780

Qy 775 GGGGTCATGCAAGAAGCAGGCATAGCAGTCAACTTTATCGAGATTGGACCGGGGAAAGTCTTG 834
         |||| ||||||||||||| || | ||| ||||||| |||||||||
Db 781 GAAACAATGCAAAAACTAGGGGCGACTCGTTTATTGAAGTGGTCCTGGGAGTACTT 840

Qy 835 TCAGTTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCG 894
         ||||| ||| | | |||| ||| | | ||| |||||| |||||||
Db 841 TCAGGTTTCATTAAGAAAAATGATAAAAAATGCAGAAAATGCGCAATGTTGCTAATGTTTAGCT 900

Qy 895 AGTTTAGTAGCACTTTTAGAAAAATA 920
         || || || ||| |||| |
Db 901 TCATTTGAAGCTTTGATTAATCAGTA 926

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; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20712
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-20712

Query Match      38.1%;  Score 350.8; DB 9; Length 927;
Best Local Similarity  61.7%;  Pred. No. 3.8e-97;
Matches  559;  Conservative  0; Mismatches 347;  Indels  0; Gaps  0;

Qy      7 AAAACAGCCTTTTATTTGCTGGTCAAGGTGCCCAGTATCGGATGGGATGGGACGGGATTTC 66
          ||||||||| ||| || ||||| |||||||||||||| || || |||||  |||||| ||
Db      4 AAAACAGCGATTTTATTTAGTGGACAAGGAGCCCAGTATCAAGGATGGGATGGTGAAGAATTA 63

Qy     67 TATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTCGGTTAT 126
          ||||||||| || ||||| || || || ||||| ||| |  ||||||||||| ||||||
Db     64 TATCACCAAGAAGCGGATTGTTCGGGAAACTTTCGATGAAGCAAGTCATATCTTAGGTTAT 123

Qy    127 GATTTACGTTATCTCATCGATACGGAAGAGACAAACTCAATCAGACCCGCTATACGCAA 186
          ||  || ||| || || ||| ||||||||| || ||||||||||   ||| ||||||
Db    124 GAGATGGCAGAACTTTGTTTTACTGAAATGAACGTTAAATGAAACAGAATATACGCAA 183

Qy    187 CCAGGCCATTCTCAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGCTATCAG 246
          |||| | |||  ||||| |||||||||||| || ||||||| ||||| |||||| ||
Db    184 CCTGCTATTTTAACAGTCAGTGTCGGCATTTTACCGTCTTTTACCGTCTTTTGCAACAAAAGGACTAACG 243

Qy    247 CCTGATATGGTTGCTGTCTTGTCTCTTGGAGAATACTCTGCCTTCGGTGCTGGCAAGCGGCGCC 306
          |||||||||||| ||||| || |||||||||| |||| ||||| ||||| ||||||||||
Db    244 CCTGATGTCGTAGCGGGGTTTAAGCTTCAGTGCTTTGGTTGGCCAGCCGGGGCT 303

Qy    307 TTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAAGAAGCG 366
          |||| |||| | ||||| || || ||  || ||| ||| ||||||||||| ||||
Db    304 TTGCGCTTTTCAGAAGCGGATTGTTCGGGAAACTTGTGGTTTGATCCAAGCAAGCAGACAGAAGCA 363

Qy    367 GCTCCTGCTGACTCTGGCAAGCATGGTAGCAGTTCTCAATACGGCCAGTAGAGGTCATTGAA 426
          |||||| ||||| ||||||| ||||| || ||||| ||| ||  || ||||| ||||
Db    364 GCACCACAAGGAACTGCAAAATGGTTGCTGTTATGAATGCTGAGCGTGAAGTAATTGAG 423

Qy    427 GAAGCCTGTCAAAAGCTTCTGAACTGGAGTGGTTACTCCAGCCAACTATAACACACCT 486
          ||| || || |||||| ||| ||| |||  || | || ||| || || ||| ||||
Db    424 AAAGCCTGCCAAGAAGCCAGTGCTTTCGGAATTGTGGCTCCAGCAAATTATAATACACCA 483

Qy    487 GCACAAATCGTTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTTTGCAA 546
          ||||||||||| |||||||| ||||| ||||| ||||||||| || |||||| ||||
Db    484 CAACAAATCGTGATTGGTGGTGAGGTTGCTGCTGTTGATCAAGCGATGACACTTTCTCAAA 543

Qy    547 GAAGCAGGTGGCCAAACGCTGATTCCTCTCTTAAGGTGTCAGTCCCCTTCACACCGCTCTC 606
          ||||||||| ||||| |||| ||| ||| || ||| | ||||| |||| ||| ||||
Db    544 GAAGCTGGTGTGAAGCGAATGATCCGTAAATGTGAGTGGCCGTGTTAGTTCTCAGGTAAGTTGAA 603

Qy    607 CTTGAGCCTGCTAGCCAGGCATTCCTGTGTAATCAGGTAAGTTTTTCAGATTTT 666
          |||||||| || |||||| || ||| || || ||  || || ||||| |||||
Db    604 TTACAACCAGCATCAAAAAAATTGGCTCAGGATTTTAGTCAAATTTCAAACGATG 663

Qy    667 ACTTGTCCCCAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAGAGGACATTGCTCAG 726
          ||||| || | |||| |||||| || || ||||| || || |||| ||||
Db    664 CAAATTCCTGTCGTTAGTAATACGACTGGTGATTAAGGCCAAATTAGGGCTAATTCAAGCG 723

Qy    727 CTCTTGAGCGCGTCAGGTCAAGGAACCCGTTCGTTGTTCTATGAAAGTATTGGGGTCATGCAA 786
          |  ||| |||||| ||||| || || ||| || || || || ||| ||| | ||||
Db    724 TTATTGGAAAAGCAAGTCATGTCTGCGGTACGTTTTGATCAGTTTGTGCTGTTGATCAAGCGATGAAG 783

Qy    787 GAAGCAGGTGCCAAAGCACTTATCGATGATTGGACCGGGAAAGTCTTGTCTCAGGTTTTGTT 846
          |||||||| || || ||  || || || ||  ||| ||||||  ||| |||| || |||||
Db    784 GCTATGAACGTAGGAACGGATGATGATTGAAGTTGGTCCAAAGGAAAAACATTAACTGGTTTTGTT 843

Qy    847 AAAAAAATTGATCAAACTGCTCACTAGCTCATGTGAAGATCAAGCGAGTTAGTAGCA 906
          || ||||||||||||||||| | ||||||| ||||| ||| || |||
Db    844 AAAAAAATGACAAACATTGAAATGAAATGACCGTGTGGAAGATGTGCAACATTAACAGAA 903

Qy    907 CTTTTA 912
          ||||||
Db    904 ACGTTA 909
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RESULT 6
US-09-134-000C-1582
; Sequence 1582, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1582

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Query Match      38.1%;  Score 350.8; DB 6; Length 948;
Best Local Similarity  61.7%;  Pred. No. 3.8e-97;
Matches  559;  Conservative  0; Mismatches 347;  Indels  0; Gaps  0;

Qy      7 AAAACAGCCTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGATGGGATGGGACGGGATTTC 66
          ||||||||| ||| || ||||| |||||||| || || || ||||| ||
Db     22 AAAACAGCGATTTTATTTATTAGTGGACAAGGAGCCCAGTATCAAGGATGGTGAAGAATTA 81

Qy     67 TATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTCGGTTAT 126
          ||||||||| || ||||| || || || ||||| ||| |  ||||||||||
Db     82 TATCACCAAGAAGCGGATTGTTCGGGAAACTTTCGATGAAGCAAGTCATATCTTAGGTTAT 141

Qy    127 GATTTACGTTATCTCATCGATACGGAAGAGACAAACTCAATCAGACCCGCTATACGCAA 186
          ||  || ||| || || ||| ||||||||| || ||||||||||
Db    142 GAGATGGCAGAACTTTGTTTTACTGAAATGAACGTTAAATGAAACAGAATATACGCAA 201

Qy    187 CTAGCCATTCTCAGCGACTTCGGTTGCTATCTACCGTTTATTGCAACAACAACACG 246
          || || |||  ||||| ||||||||||| || ||||||| || ||
Db    202 CCTGCTATTTTAACAGTCAGTGTCGCCATTTTACCGTCTTTTGCAACAAAAGGACTAACG 261

Qy    247 CCTGATATGGTTGCTGTTGTCTCTTCTGGAGAATACTCTGCCTTGGTGCCTTGGGTCGGCGCC 306
          |||||||||||| ||||| || ||||| |||||| || ||||| ||||
Db    262 CCTGATGTCGTAGCGGGGTTTAAGCTTCAGTGCTTTGGTTTGGTTGTTCCAGGGGGCT 321

Qy    307 TTGGATTTGAAGATGCGGTTGCCTTGGTGTGGCCTATATGGAAGAAGCG 366
          |||| |||| | |||| || || ||  || ||||||||||| ||||
Db    322 TTGCGCTTTTCAGAAGCGGATTGGCGGTAGCAGTGGCCGTCAGTACATGACAGAAGCA 381

Qy    367 GCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGGCCAGTAGAGGTCATTGAA 426
          |||||| ||||| ||||||| ||||| || ||| ||  || ||||| ||||
Db    382 GCACCACAAGGAACTGGCAAAATGGTTGCTGTTATGAATGGTTGTTATGAATGCTGAAGTAATTGAG 441

Qy    427 GAAGCCTGTCAAAAGCTTCTGAACTGCTGTGATGCAAAAGAGGACAGTTGCTCAG 486
          ||| || || |||||| ||| ||| || |||| || |||| || ||||
Db    442 AAAGCCTGCCAAGAAGCCAGTGCTTTCGGAATTGTGGCTCCAGCAAATTATAATACACCA 501

Qy    487 GCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTTTGCAA 546
          |||||||| || |||| || ||||| ||||| ||||||| || |||||| ||||
Db    502 CAACAAATCGTGATTGGTGGTGCTGTTGATCAAGCGATGACACTTTCTCAAA 561

Qy    547 GAAGCAGGTGCCAAACGCTTGATTCCTTCTTAAGGTGTCAGTCCCTTTCACACCGCCTCTC 606
          ||||||||| ||||| || ||| ||| || ||| | ||||| |||| ||| ||||
Db    562 GAAGCTGGTGTGAAGCGAATGATTCCGTAAATGTGAGTGGCCCTTTCCCATACGGCGCTG 621

Qy    607 CTTGAGCCTGCTAGCCAGGAACTAGCTCATGTGAAGATCAAGCGAGTTAGTAGCA 666
          |||||||| || |||||||
Db    607
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Db    622  TTACAACCAGCATCAAAAAAATTGGCTCAGGATTTAGCAACATTGAACTTTCAAACGATG  681
                 |||| ||| |||||||   ||||||||| ||  |  ||| |||||   |||
Qy    667  ACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGACATTGCTCAG  726
                 |  ||| ||||| |||||   | ||||||||| |||  |||||| |||||
Db    682  CAAATTCCTGTCGTCATTAGTAATACGACTGCCGAAATTATGCCCCAAGAGAGGCAATTCAAGCG  741

Qy    727  CTCTTGACGCGTCAGGTCAGGTCAAGGAACCCGTTCGTTCTTCATGAAAGTATTGGGGTCATGCAA  786
                 |  ||| ||   |||  |||  |||||     |||| ||||  ||||||||
Db    742  TTATTGGAAAAGCAAGTCAGTCATGTCTGCGGTACGTTTTGAAGACCAGTATCGGAAACGATGAAG  801

Qy    787  GAAGCAGGCATAAGCAACTTATCGAGATGGACCGGGGAAAGTCTTGCTGTGTCAGTTTTGTT  846
                 ||  ||||     | ||   |||||||  ||||| |  |||||   ||||
Db    802  GCTATGACGTAGGAACGAGTGAAGTTGGTCCAGGGAAAAACATTAACTGGTTTTGTT  861

Qy    847  AAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTAGTAGCA  906
                 ||||||||||||||||||   |||||||||||||||||||||||||||
Db    862  AAAAAATTGACAAAACAATTGAAATGCACCGTGTGGAAGATGTTGCAACATTAACAGAA  921

Qy    907  CTTTTA  912
                 ||
Db    922  ACGTTA  927
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RESULT 7
US-09-134-000C-1582
; Sequence 1582, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1582

Query Match   38.1%; Score 350.8; DB 6; Length 948;
Best Local Similarity 61.7%; Pred. No. 3.8e-97;
Matches 559; Conservative   0; Mismatches 347; Indels   0; Gaps   0;

```
Qy      7  AAAACAGCCTTTTATTTGCTGTCAAGGTGCCCAGTATCTAGGGATGGGACGGGGATTTC  66
                |||||||||   ||||||||||||||||||||||||
Db     22  AAAACAGCGATTTTATTTAGTTGGACAAGGAGCCCAGTATCAAGGGATGGGTGAAGAATTA  81

Qy     67  TATGATCAGTAGTCATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTGCTGCTCGGTTAT  126
                ||||||||||||||||||   |||||||| ||| |||||||||||||
Db     82  TATCACCAAGAGAGCGATTGTTCGGGAACTTTCGATGAAGCAAGTCATATATCTTAGGTTAT  141

Qy    127  GATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACACCCGCTATACGCAA  186
                ||| |||||||||||||||||  |||||||| |||||||||||
Db    142  GAGATGGCAGAACTTGTTTTACTCGAAAATGAACGTTTAAATGAAACAGAATATACGGCAA  201

Qy    187  CCAGCCATTCTAGGACTTCGGTTGCTATCTACCGTTTATTACCGTTTACCGTCTTTTACCGT  246
                |||| ||||||  || ||  ||||||  |||||||| ||||||||
Db    202  CCTGCTATTTAACAGTGGTTGCTGGTTTCTCTTGGAGAATACTCTGCCTTGGTGTGCCAGCGGCGCC  306

Qy    247  CCTGATATGGTTCGTAGCGGGGTTTAAGCTTAGGGAATACAGTGCTTTGGTTGCCAGCGGCT  306
                |||||||||||||||||||||||||||   |||||||||
Db    262  CCTGATGTCGTAGCGGGGTTTAAGCTTAGGGAATACAGTGCTTTGGTTGCCAGCGGCT  366

Qy    307  TTGGATTTTGAAGATGCGATTTTATTTAGTTAGTGGACAAGGAGCCTATATGGAAGAAGCG  366
                |||||||||||||||||| ||||  |||||||||||
Db    322  TTGCGCTTTTCAGAAGCCGATTGTTCGGGTCCAAAAGCGCGGTCAGTACATGACAGAAGCA  381

Qy    367  GCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACCGCCAGTAGAGAGTCATTGAA  426
                |  |||||||||||||||||  ||||||||||||  ||||| ||||||||||||
Db    427  GAAGCCGTGCTCAAAAAGCTTCTGAACTGGAGTGGTTACTCCAGCGACTGGGTTGCGTGAAGCTGAGCGCAACTACACCCT  486
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(Lower right region)

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Db    382  GCACCACAAGGAACTGGCAAAATGGTGCTGTTATGAATGCTGAGCGTGAGCGTGAAGTAATTGAG  441

Qy    427  GAAGCCGTGCTCAAAAAGCTTCTGAACTGGAGTGGTTACTCCAGCGACTAAACACCCT  486
                ||||| |||||||||||||||||||||  |||||||||||||||||||||
Db    442  AAAGCCTGCCAAGAAGCCAGTGCTTCCGGAATTGTGGCTCCAGCAAATATTAATACACCA  501

Qy    487  GCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTGACGCGGTTGAACTTTGCAA  546
                |||||||||||||| ||||||||||||||||||||||||||
Db    502  CAACAAATCGTGATTGTGGTGGTGGTGCTGTGTGATCAAGGCGATGACACTTCTCAAA  561

Qy    547  GAAGCAGGTGCCAAAGCTTGATTCGTCAGTGTGTGTCTTGCTGTGTCAGTTTTGTT  606
                |||||  ||||||||||| | | || |||||||||   |||||   ||||
Db    562  GAAGCTGGTGTGAAGCGAATGATTCCGTTAAATGTGAGTGGCCCTTTCCATACGGCGGTG  621

Qy    607  CTTGAGCGTGTAGCCAGAAACTAGCTGAAGATCAAGCCAGTTGAAGTTTTCAGATTTT  666
                |||  ||| |||||   ||  |||||  ||| | |||||   |||||
Db    622  TTACAACCAGCATCAAAAAAATTGGCTCAGGATTTAGCAACATTGAACTTTCAAACGATG  681

Qy    667  ACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGACATTGCTCAG  726
                |  ||| ||||| |||||   | ||||||||| |||  |||||| |||||
Db    682  CAAATTCCTGTCGTCATTAGTAATACGACTGCCGAAATTATGCCCCAAGAGAGGCAATTCAAGCG  741

Qy    727  CTCTTGACGCGTCAGGTCAGGTCAAGGAACCCGTTCGTTCTTCATGAAAGTATTGGGGTCATGCAA  786
                |  ||| ||   |||  |||  |||||     |||| ||||  ||||||||
Db    742  TTATTGGAAAAGCAAGTCAGTCATGTCTGCGGTACGTTTTGAAGACCAGTATCGGAAACGATGAAG  801

Qy    787  GAAGCAGGCATAAGCAACTTATCGAGATGGACCGGGGAAAGTCTTGCTGTGTCAGTTTTGTT  846
                ||  ||||     | ||   |||||||  ||||| |  |||||   ||||
Db    802  GCTATGACGTAGGAACGAGTGAAGTTGGTCCAGGGAAAAACATTAACTGGTTTTGTT  861

Qy    847  AAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTAGTAGCA  906
                ||||||||||||||||||   |||||||||||||||||||||||||||
Db    862  AAAAAATTGACAAAACAATTGAAATGCACCGTGTGGAAGATGTTGCAACATTAACAGAA  921

Qy    907  CTTTTA  912
                ||
Db    922  ACGTTA  927
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RESULT 8
US-10-434-665-1582
; Sequence 1582, Application US/10434665
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-09
; CURRENT APPLICATION NUMBER: US/10/434,665
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 09/134,000
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-434-665-1582

Query Match   38.1%; Score 350.8; DB 8; Length 948;
Best Local Similarity 61.7%; Pred. No. 3.8e-97;
Matches 559; Conservative   0; Mismatches 347; Indels   0; Gaps   0;

```
Qy      7  AAAACAGCCTTTTATTTGCTGTCAAGGTGCCCAGTATCTAGGGATGGGACGGGGATTTC  66
                |||||||||   ||||||||||||||||||||||||
Db     22  AAAACAGCGATTTTATTTAGTTGGACAAGGAGCCCAGTATCAAGGGATGGGTGAAGAATTA  81

Qy     67  TATGATCAGTAGTCATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTGCTGCTCGGTTAT  126
                ||||||||||||||||||   |||||||| ||| |||||||||||||
Db     82  TATCACCAAGAGAGCGATTGTTCGGGAACTTTCGATGAAGCAAGTCATATATCTTAGGTTAT  141
```

APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21491
LENGTH: 915
TYPE: DNA
ORGANISM: Enterococcus faecium
US-10-282-122A-21491

Query Match   34.4%; Score 316.8; DB 9; Length 915;
Best Local Similarity   60.0%; Pred. No. 1.1e-86;
Matches 547; Conservative   0; Mismatches 362; Indels   3; Gaps   1;

Qy   7 AAAACAGCCTTTTATTTGCTGGTCAAGGTGCCCAGTATCTTAGGGATGGGACGGGATTTC   66
            ||||||| ||| || ||||| | ||||||| || ||| ||||||| |||| |||| |||
Db   4 AAAACAGCATTCTTATTTAGTGGCCAAGGTGCACAATATATCAAGGTATGGGAAAAGATTTA   63

Qy   67 TATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGTGCTCCGTTAT   126
            || ||||||| || || || | || || |||| ||| |||||| || || ||| ||
Db   64 TATGAAGAAG--CCGTTGTAAAGCAGACATTTGATGAAGCAGAGTGAGATTCTCCGGCTAC   120

Qy   127 GATTTACGTTATCTCATCGATACGGAAGAAGAGAGAAAACTCAATCAGACCCGCTATACGCAA   186
            || |||| |||| | ||| |||| |||| || || | | ||| ||| | | | ||||
Db   121 GATAATGGCTGAACTTTGCTTTACAGAAAATGAACGTTGGATCCGTTATTCGCTTATTGAAGA   180

Qy   187 CCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTATTGCAAGAAAAGGGCTATCAG   246
            |||| | |||| |||| | |||| | || || ||||| | |||| ||| ||||| ||||
Db   181 CCAGCTATTCTAACAGTCAGCATGCTCAGCTTGGTGAGAATATTCGGCATTAGTAGTAATGCG   240

Qy   247 CCTGATATGGTTGCTGGTTGTCTCTTGGAGAATACTCTGCCTTGGTGTGCAAGCGCGCC   306
            |||| ||| | |||| ||| | ||||| || || | ||| ||| || ||| || ||
Db   241 CCAGATGCAGCTTTAGGACTGAGTTTAGGAGGAATATTGACAGAGCT   300

Qy   307 TTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGAGCCTATATGGAAGAAGACGG   366
            ||| |||| ||| |||| | || |||| | |||| |||| |||||||| || ||||
Db   301 CTATCCTTCACTGAAGCAGTTGCGTTAGTAGCAGAAAAAGAGGCGCCTTATATGACAGAAGCT   360

Qy   367 GCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTCATTGAA   426
            |||| ||| ||| || || ||| | ||| || |||| ||||| || || || |||||||
Db   361 GCCCCAGCTGCAGCGGGAAAATGGTTGCAGTGAGCCGATTGAATGCCGATTGAAACGATCGAG   420

Qy   427 GAAGCCTGTCAAAAAGCTTCTGAACTTGGACGTGGTTACTTCCAGCCAACTATAACACACCT   486
            |||| ||| || |||| ||||||| |||| |||| ||||| ||| | || | |||| ||
Db   421 GAAAGCTCATGAGGCTAGCAAGTACGGACCATCGTATCCTCCGAAATTATAATACACCT   480

Qy   487 GCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGTGAACTTTTGCAA   546
            |||| || ||||| || ||| || || || || || || |||| || || || |||
Db   481 CAGCAGATCGATTGGTGCGGAGAAAAAGCAGTAGACGAGGAAGCGTGTTTTACTATTAAAA   540

Qy   127 GATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTATACGCAA   186
            || | | |||| |||| ||||| || |||| || || ||| | | |||||
Db   142 GAGATGGCAGAACGTTTGTTTTACTGAAAATGAACGTTAAAATGAAACAGAATACGCAA   201

Qy   187 CCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTATTGCAAGAAAAGGGCTATCAG   246
            ||||| || |||| || | || | | |||| ||||| |||| ||| ||| ||||||
Db   202 CCTGCTATTTTAACAGTCAGTGTCGCATTTTACCGTCTTTTCCAACAAAAGGACTAACG   261

Qy   247 CCTGATATGGTTGCTGGTTGTCTCTTGGAGAATACTCTGGCAAGCGCGGGCGCC   306
            ||||| ||| | |||| || | |||| || || | || || | ||| | ||
Db   262 CCTGATGTCGTAGCGCGGGTTAAGCTTAGGGGAATACAGTGCTTTGGTTGCCAGCGGGGCT   321

Qy   307 TTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGAGCCTATATGGAAGAAGACGG   366
            || |||| ||| ||| | ||| || || | ||| | || | ||||||| ||||
Db   322 TTGCGCTTTTCAGAAGCAGTGCGGCCTTGTCCAAAAGCGCGGTCAGTACATGACAGAAGCA   381

Qy   367 GCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTCATTGAG   426
            |||| ||| ||| || || ||| | ||| || |||| ||||| || || || ||||| |
Db   382 GCACCACAAGGAACTGGCAAAATGGTTGCGTCTGCTTATGGAATGCTGAGCCGTGAGTAATTGAG   441

Qy   427 GAAGCCTGTCAAAAAGCTTCTGAACTTGGACGTGGTTACTTCCAGCCAACTATAACACACCT   486
            |||| ||| || |||| ||||||| ||| |||| | ||| | || || | | |||| |
Db   442 AAAGCCTGCCAAGAAGCCAGTGCTGCTTTTCGGAATTGTGTGCTCCAGCAAATTATAATAATGAACTACCA   501

Qy   487 GCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGTGAACTTTTGCAA   546
            |||| || ||||| || ||| || || || || | |||| | ||| || || || ||
Db   502 CAACAAATCGTGATTGGTGAGGTTGCTGCTTGTGTGCGTGATCAAGCGATGACAACTTTCTCAA   561

Qy   547 GAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTGCCCTTTCACCCGCTCTC   606
            |||| || || || || | || || || |||| |||| || | ||| ||| | ||
Db   562 GAAGCTGGTGTGAAGCGAATGATTCCGTAAAATGTGAGTGGCCCTTTCCATACGGCGCTG   621

Qy   607 CTTGAGCCTGCTGCCCAGAAACTAGCTGAAAACTCAGCTCAGTGAGTTGCGATTTT   666
            || || || | || ||| || ||| || | ||| | |||||| ||||
Db   622 TTACAACGATCATCAACAAAAAAAATTGGCTCCAGGATTTAGCAAAATTGAACTTTCAAACGATG   681

Qy   667 ACTTGTCCCCTAGTCGGCAATACAGAGCGTGCTGTGATGCAAAAGAGGACATTGCTCAG   726
            ||||| || || || || ||| ||||| ||| || |||| ||| | || ||| ||||
Db   682 CAAATTCCTGTCATTAGTAATACGACTGCCGAAATTATGCCCCAGAGGCAATTCAAGCG   741

Qy   727 CTCTTGACGCGTCAGGTCAGGAACCCGTTCGTTCTATGAAGTATTGGGGTCATGCAA   786
            || | || | | ||| | || || | ||| | |||| | | | ||| ||||
Db   742 TTATTGGAAAAGCAAGTCAAGTGTGTCGCGGTACGGTTTGAAGACAGATCGAAACGATGAAG   801

Qy   787 GAAGCAGGCATAAGCAACTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGTTTTGTT   846
            ||||| ||| | | | | |||| || || | || ||| | | | || |||||||
Db   802 GCTATGAACGTAGGACGATGAAGTTGGTCCAGGGAAAACATTAACTGTTTTTGTT   861

Qy   847 AAAAAAATTGATCAAACTGCTCACTTACTGCTCATGTGGAAGATCAAGCGAGTTTAGTAGCA   906
            ||| || ||||| ||| | | || | ||| || | || |||| ||| ||||| |||| |
Db   862 AAAAAATTGACAAAACATTGAAATGCACCGTGTTGCCAGAGATGTTGCAAGATTAACAGAA   921

Qy   907 CTTTTA   912
            ||| |
Db   922 ACGTTA   927

RESULT 9
US-10-282-122A-21491
Sequence 21491, Application US/10282122A
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

```
   MOLECULE TYPE: DNA (genomic)
   HYPOTHETICAL: NO
   ANTI-SENSE: NO
   ORIGINAL SOURCE:
     ORGANISM: Enterococcus faecium
   FEATURE:
     NAME/KEY: misc_feature
     LOCATION: (B) LOCATION 1...987
   SEQUENCE DESCRIPTION: SEQ ID NO: 3319:
US-10-417-884-3319

Query Match         34.2%;  Score 315.2;  DB 8;  Length 987;
Best Local Similarity   59.9%;  Pred. No. 3.7e-86;
Matches  546;  Conservative  0;  Mismatches  363;  Indels  3;  Gaps  1;

Qy      7 AAAACAGCCTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGGCGATTTC  66
            ||||||| ||||| |||||  ||||  ||||||||| |||||| ||||||||| ||   |
Db     73 AAAACAGCATTCTTATTTAGTGGCCAAGGTGCCACATATCAAGGTATGGGAAAAGATTTA 132

Qy     67 TATGATCAGTATCCGATTGTCAAGAAACGATTGATCGAGCGAGTCAGTGTCTCGGTTAT  126
            ||||| |||     ||||||||||| || ||| ||||| |||| |||| ||| ||| ||
Db    133 TATGAAGAAG--CCGTTGTAAGCAGCAGAAATCGAAGCAAGCAGTTGAGATTCTCGGCTAC 189

Qy    127 GATTTACGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGTATACGCAA  186
            |||  |||  | ||||  || |||  ||  |||||  | |||||   ||  ||||| |||
Db    190 GATAGGCTGAACTTGCTTTACAGAAAATGAACGTTGGATCAGACGCAATATACACAG 249

Qy    187 CCAGCCATTCTAGCGACTTCGGTTGCTATCTCGGTATTGCTTATTGCAAGAAGGAGCATG  246
            ||||||||| || || || ||||||||||  |||  | ||||||||  ||||| ||  |
Db    250 CCAGCCATTCTAACAGTCAACGATCGGCATCGGTATTATCGCTTATTGGAAGAAGGAGCATG 309

Qy    247 CCTGATATGGTTGCTCTGTTGTCCTCTGGAGAATACCTGCCTTGGTGGCAAGCGGCCGCC  306
            |||||||| |||||| | |||||||  || |||| ||| | |||||||||   ||||  |
Db    310 CCAGATGCAGCTTAGGACTGAGTTTAGGAGAATATTCGGCATTAGTAGCTGTAATGCG 369

Qy    307 TTGGATTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTCATATGGAAGAGCG  366
            | |||||| || ||| |||||||| ||||| ||||| |||| ||  |||||||||||||
Db    370 CTATCCTTCACTGAAGCAGTTGCGTTAGTAGCAGCAAAAGAGAGCGCTATATGACAGAAGCT 429

Qy    367 GCTCCTGCTGACTCTGGCGAAGATGAGTAGCAGTTCTCAATACGCCAGTAGAGGTCATTGAA  426
            |||  ||||||||  || ||| ||| || ||  | |  | || | ||| || |||||||||
Db    430 ACCCCAGCTGGAAGCGGAAAATGGTTGCAGTGATGATGAATGGCCGATTGAAACGATCGAG 489

Qy    427 GAAGCCTGTCAAAAGTTCTGAACTTGGAGTGGTTACTCAGCCAACTATAACACACCT  486
            |||| | ||||||||||  || |||| ||  ||||| ||||||| || |||| |||||
Db    490 GAAAGCTGTCATCGAAGCTAGCAAGTACGGCATCGTATCTCCTGCAAATTATAATAACACCT 549

Qy    487 GCACAAATCGTCATTGCTGCGGAGAAGGTTGTTGCAGTTGATGAGCGCGGTTGAACTTTTGCAA  546
            ||||||| |||| ||||| | |||| || ||  | ||| ||||| |||||| ||||| ||||||
Db    550 CAGCAGATCGTGATTGGTGGCGAAGAAAAGCAGTAGACGAGCTGTTTCTACTATTAAAA 609

Qy    547 GAAGCAGGTGCCAAACGCTGATTCCTCTTAAGGTGTGTCAGGTCCCTTTCACACCGCTCTC  606
            |||  ||| ||||| |  |||| ||||||||  || |||||| |||||||||| ||| ||
Db    610 GAAAAAGGGTTCAAAGAATGATCCCTCTAAATGTCAGCGGGCCTTTTCATACAGCTATT 669

Qy    607 CTTGAGCCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTCAGATTTT  666
            |||||||| ||| ||||| |||| |||  || || |||||  || ||||||||  | ||
Db    670 TTAGAACCGGCAGCAAAAAACTGGCGAGGAGGACCTAAGTCAGATTCAATTCTCTGAACCT 729

Qy    667 ACTTGTCCCCTAGTCGGCAATACAGAGAGTGCTGTGATGCAAATAATGAAGAAACAATCGCGGGA  726
            ||||  |||  | |  ||||| || ||||| | |||||||||||||||||||||| |||||||||
Db    730 TCTTTTCCTATCATAAGCAACAACACGAAATAATGAAGAAAGAAACAATCGCGGGA 789

Qy    727 CTCTTGACGCGGTCAGGTCAAGGAACCGTTCGTTCGTTTCGTTCTATGAAAGTATCATCAAGTAAGTTAAAA  786
            |  ||||| || |||| ||||||||||| || ||  || ||| ||||| |||| | ||| ||||||| ||||
Db    790 CTACTTGAACAGCAAGCAACTTATCGAGATTGACCGGGCGGCCCCCGGAAAAGTATTAAGCCGAGTTTAGTAGCA 849

Qy    787 GAAGCAGGCATAAGCAACTTATCGAGATTGACCGGGCGGCCCCCGGAAAAGTATTAAGCCGAGTTTTGTT  846
            |||||| |||||||||||| |  | |||||||| | || ||||  ||||| ||||||||||||||| ||
Db    850 ACAATCGGCATCGAACAAGTCATCGAAGTCATCGAAGTGGAAGATCTGGAAATAAGCAGACATTTGATGAA 909

Qy    847 AAAAAATTGATCAAACTGCTCACTTAGCTCATGTGAAGATCAAGCGAGTTTAGTAGCA  906
            ||||||||||| || |||||||  |||  | |||||||| |||| |||||||||||||
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Qy    547 GAAGCAGGTGCCAAACGCTGATTCCTCTTAAGGTGTGTCAGGTCCCTTTCACACCGCTCTC  606
            |||  ||| ||||| |  |||| ||||||||  || |||||| |||||||||| ||| ||
Db    541 GAAAAAGGGTTCAAAGAATGATCCCTCTAAATGTCAGCGGGCCTTTTCATACAGCTATT 600

Qy    607 CTTGAGCCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTCAGATTTT  666
            |||||||| ||| ||||| |||| |||  || || |||||  || ||||||||  | ||
Db    601 TTAGAACCGGCAGCAAAAAACTGGCGAGGAGGACCTAAGTCAGATTCAATTCTCTGAACCT 660

Qy    667 ACTTGTCCCCTAGTCGGCAATACAGAGAGTGCTGTGATGCAAATAATGAAGAAACAATCGCGGGA  726
            ||||  |||  | |  ||||| || ||||| | |||||||||||||||||||||| |||||||||
Db    661 TCTTTTCCTATCATAAGCAACAACACGGAAATAATGAAGAAAGAAACAATCGCGGGA 720

Qy    727 CTCTTGACGCGGTCAGGTCAAGGAACCGTTCGTTCGTTTCGTTCTATGAAAGTATCATCAAGTAAGTTAAAA  786
            |  ||||| || |||| ||||||||||| || ||  || ||| ||||| |||| | ||| ||||||| ||||
Db    721 CTACTTGAACAGCAAGCAACTTATCGAGATTGACCGGGCGGCCCCCGGAAAAGTATTAAGCCGAGTTTAGTAGCA 780

Qy    787 GAAGCAGGCATAAGCAACTTATCGAGATTGACCGGGCGGCCCCCGGAAAAGTATTAAGCCGAGTTTTGTT  846
            |||||| |||||||||||| |  | |||||||| | || ||||  ||||| ||||||||||||||| ||
Db    781 ACAATCGGCATCGAACAAGTCATCGAAGTCATCGAAGTGGAAGATCTGGAAATAAGCAGACATTTATG 840

Qy    847 AAAAAATTGATCAAACTGCTCACTTAGCTCATGTGAAGATCAAGCGAGTTTAGTAGCA  906
            ||||||||||| || |||||||  |||  | |||||||| |||| |||||||||||||
Db    841 AAAAAATCGATAAAACAATACCAGTTCTGCGTGTTGAGAATAAGCAGCACATTTGATGAA 900

Qy    907 CTTTAGAAAAA  918
            | |||| ||||
Db    901 ACAATAGCAATA 912
```

RESULT 10
US-10-417-884-3319
; Sequence 3319, Application US/10417884
; GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
  ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
  ADDRESSEE: GENOME THERAPEUTICS CORPORATION
  STREET: 100 Beaver Street
  CITY: Waltham
  STATE: Massachusetts
  COUNTRY: USA
  ZIP: 02354
COMPUTER READABLE FORM:
  MEDIUM TYPE: CD/ROM ISO9660
  COMPUTER: PC
  OPERATING SYSTEM: <Unknown>
  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/417,884
  FILING DATE: 17-Apr-2003
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/107,532A
  FILING DATE: 30-Jun-1998
  APPLICATION NUMBER: 60/085,598
  FILING DATE: 14 May 1998
  APPLICATION NUMBER: 60/051571
  FILING DAT: July 2, 1997
ATTORNEY/AGENT INFORMATION:
  NAME: Ariniello, Pamela Deneke
  REGISTRATION NUMBER: 40,489
  REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (781)893-5007
  TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3319:
SEQUENCE CHARACTERISTICS:
  LENGTH: 987 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: double
  TOPOLOGY: circular

```
Db   196  CGTACTCAACCTGCGTTGCTTGCGTGTGTATGCGCAAGTG  255
          ||||||||||||||||||||||||||||||||||||||||
Qy   238  GG---CTATCAGCCTGATATGGTTGTCTTGTCTTGGTG  294
          ||||    |||||||||||||||||||||||||
Db   256  GGTCTTGAGCAACCTGCGGTTTAGCTGGTGGTGGTGAATATTCAGCACTGGTA  315

Qy   295  GCAAGCGGCGGCCTTGGATTTGAAGATGCGGTTGCCTTGTGTAGCTGA  354
          ||||||||||||||||||||||||||||||||||||||||||||||
Db   316  TGTGCGGCGGCTGATTGATTTTAAACAAGCGATCAAGCTCGTGGTGGTCAATTG  375

Qy   355  ATGGAAGAAGCGGGTCCTGCTGACTCTGCCAAGATGGTAGCAGTTCTCAATACGGCCAGTA  414
          ||||||||||||||||||||||||||||||||||||||||||||
Db   376  ATGCAACAAGGGTGCCTGCCGGTACGGGTGCAATGTACCGATCATCGGTCTAGAAGAT  435

Qy   415  GAGGTCATTGAAGAAGCCTGTCAAAAGCTTCTGAGTGGTGTTACTCCAGCCAAC  474
          |||||||||||||||||||||||||||||||||
Db   436  GAAGCGGATTGCTAAAGCCTGTGCTGCGCAGGTGAAGTGGTTTCTCCTGTAAAC  495

Qy   475  TATAACACCTGCACAAATCGTCATTGCTGGAGAGAGTGGTTGCAGTTGATCGAGCGGTT  534
          |||||||||||||||||||||||||||||||
Db   496  TTTAACTCACCAGGCCAAGTGGTTATTGCTGGTCAAAAGATGCGGTTGAGCGTCGCGGC  555

Qy   535  GAACTTTGCAAGAAGCAGGTGCCAAACGTTGATTCCTCTTAAGGTGTCAGGTGTCCCTTT  594
          |||||||||||||||||||||||||||||||
Db   556  GTTCTCGTGTAAAGAAGAGGCGGGGCGAAACGTGCGCTGCCTCTGCCGTTCCGTACCATCA  615

Qy   595  CACACCGCTCTCCTTGAGCCTGCTAGCCACAGAAACTAGCTGAAACTCTAGTCAGGTAAGT  654
          ||||||||||||||||||||||||||||||
Db   616  CACTGCGCCGTTGATGCAGCTCGCTGCCGATGAATTGGCAAAACTCAGCAGAGTTGAA  675

Qy   655  TTTCAGATTTTACTTGTCCCCAGTCGGCAATACAGAAGCT---GCTGTGATGCAAAAA  711
          ||||||||||||||||||||||||
Db   676  TTCAATGCACCACAAATTCCGGTCATCAATAACGTTGATGTTGTGCTGAAACCGATCCG  735

Qy   712  GAGGACATTGCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTCTCTGATGAAAGT  771
          ||||||||||||||||||||||||||
Db   736  GTAAAAATTAAAGATGCGTTGATTCGTCAACTCTATAGCCCAGTTCGTTGGACTGAATGC  795

Qy   772  ATTGGGTCATGCAAGAGCAGGCATAAGCTTTATCGAGATTGGACCGGGGAAAGTC  831
          ||||||||||||||||
Db   796  GTTGAACAAATGAGCGCACAAGGTGCACAAGGTGTGAAAAGCTGATTGAAAAGTGCTAAGTA  855

Qy   832  TTGTCAGGTTTGTTAAAAAATTGATCAAAC  863
          ||| |||||||||||||
Db   856  TTGACTGGTCTAACAAAACGTATTGTAAAAAC  887
```

```
RESULT 11
US-10-282-122A-41191
; Sequence 41191, Application US/10282122A
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT: Zamudio, Carlos
;  APPLICANT: Malone, Cheryl
;  APPLICANT: Haselbeck, Robert
;  APPLICANT: Ohlsen, Kari
;  APPLICANT: Zyskind, Judith
;  APPLICANT: Wall, Daniel
;  APPLICANT: Trawick, John
;  APPLICANT: Carr, Grant
;  APPLICANT: Yamamoto, Robert
;  APPLICANT: Forsyth, R.
;  APPLICANT: Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 41191
;  LENGTH: 939
;  TYPE: DNA
;  ORGANISM: Vibrio cholerae
US-10-282-122A-41191

Query Match   23.6%;  Score 217.6;  DB 9;  Length 939;
Best Local Similarity   55.5%;  Pred. No. 4.3e-56;
Matches  484;  Conservative  0;  Mismatches 379;  Indels  9;  Gaps  3;

Qy    1  ATGACTAAAACAGCCCTTTTATTTGCTGGTCAAGGTGCCAGTATCTAGGGATGGGACGG  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   16  ATGAGTAAGTTGCTATCGTATTCCAGGTCAGGGCTCGCAAGCAGGAGGTATGCTGGCT  75

Qy   61  GGATTTCTATGATGATCAGTATCCGATTGTCAAGAAACGATTGATCGAGCGAGTCAGGTGCTC  120
         |||| |||||||||||||||||||||| |||
Db   76  GACCTTGCCGAGCAGTATGCTGTGGTAAACAAATTCGCCGAAGCTTCAGAAGTGCTT  135

Qy  121  GGTTATGATTTAGTTAGTTATCTCATC---GATACGGAAGAAGACAAACTCAATCAGACCCGC  177
         |||||||||||||||||||      |||||||||||||||
Db  136  GGTTACGGATCTGTGGGGCGTGGTTCAAGAATGGCCCTGTGGAAGATCTCAACCAAACTTTC  195

Qy  178  TATACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAG  237
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RESULT 12
US-10-282-122A-32186
; Sequence 32186, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

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Db   907  CTTTTAGAAAAA  918
          |||| ||||
Db   970  ACAATAGCAATA  981

Qy   910  AAAAAAATCGATAAAACAATACCAGTTCTGCGTGGTGTGAGAATAAGCAGACATTTGATGAA  969
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Db   661 TTTAAACAACCTGAAATTCAAGTTGTTAATAANTGTGATGTGAAAGACACAACCGATGCT 720
             ||||  |||||||             ||| |||    |||  |||   |||
Qy   712 GAGGACATTGCTCAGCTCTTGACGCGTCAGTCAGGTCAAGAAGCACAACCGTTCGTTTCTTATGAAAGT 771
Db   721 AATGCTATTCGAGATGCATTAGTTCGTCAGCTTTATAACCCAGTCCCGTGGACTGAAACG 780
             |||||||||  ||  ||  ||||| ||  |||||| |||  ||| | |||||
Qy   772 ATTGGGGTCATGCAAGAAGCAGCATAAGCACTTATCGAGATTGACCGGGGAAAGTC 831
Db   781 GTTGAATTATTGCTGCTGTAAGGGCATCACACAATTATTAGAAATAGGACCCGTAAAGTA 840
             |||                     |||             ||| ||| |||
Qy   832 TTGTCAGGTTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAA 891
Db   841 TTAACTGTTTAACGAAACGTATTTCAAAGAGATGAACGCTGCAGCAGTTAATGATATT 900
             |||                          |||  |||  |||
Qy   892 GCGAGTTTAGTAGCACTTTAGAAAA 917
             || ||||            |||
Db   901 GCATCATTAGACCGCTGCATTAGGAAA 926
```

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RESULT 13
US-10-282-122A-21907
; Sequence 21907, Application US/10282122A
; GENERAL INFORMATION:
;    APPLICANT: Wang, Liangsu
;    APPLICANT: Zamudio, Carlos
;    APPLICANT: Malone, Cheryl
;    APPLICANT: Haselbeck, Robert
;    APPLICANT: Chlsen, Karl
;    APPLICANT: Zyskind, Judith
;    APPLICANT: Wall, Daniel
;    APPLICANT: Trawick, John
;    APPLICANT: Carr, Grant
;    APPLICANT: Yamamoto, Robert
;    APPLICANT: Forsyth, R.
;    APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE:  2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE:  2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE:  2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE:  2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE:  2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE:  2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE:  2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE:  2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE:  2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE:  2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE:  2001-02-16
; Remaining Prior Application data removed  -  See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21907
;   LENGTH: 939
;   TYPE: DNA
;   ORGANISM: Haemophilus influenzae
US-10-282-122A-21907

Query Match             21.3%;  Score 196.4;  DB 9;  Length 939;
Best Local Similarity   54.1%;  Pred. No. 1.5e-49;
Matches  470;  Conservative   0;  Mismatches 386;  Indels   12;  Gaps   3;
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; PRIOR FILING DATE:  2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE:  2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE:  2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE:  2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE:  2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE:  2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE:  2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE:  2001-02-16
; Remaining Prior Application data removed  -  See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32186
;   LENGTH: 930
;   TYPE: DNA
;   ORGANISM: Proteus mirabilis
US-10-282-122A-32186

Query Match             21.3%;  Score 196.4;  DB 9;  Length 930;
Best Local Similarity   53.0%;  Pred. No. 1.5e-49;
Matches  491;  Conservative   0;  Mismatches 426;  Indels   9;  Gaps   3;

Qy     1 ATGACTAAAACAGCCTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 60
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Db     1 ATGACTGATTTGCAATGGTTTTCCCTGGACAGGATCACAAGCGATTGGAAATGCTTGCA 60

Qy    61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
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Db    61 GAACTTGCCGAGCATTATCCAATAGTGACAGAAACATTTGCTCAAGCATCTGATGTATTG 120

Qy   121 GGTTATGATTTACGTTATCTCATCGATCGGAA---GAAGACAAACTCAATCAGACCCGC 177
           ||||                   ||||| |||   ||| ||||  ||||| || |||
Db   121 GGTTATTCTCTTTGGGATTTAGTGCAAAATGGTCCTGAGAGAAGAGTTAAACAAACATGG 180

Qy   178 TATACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAA-- 235
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Db   181 AAAACACAGCCGGCATTATTAGCAGCAGCCATCCGTTGCTATTGGGGAGTATGGCAAGAAAAA 240

Qy   236 -AGGGCTATCAGCCTGATATGGTTGTCTGTTGTTTGTCTTGGAGAAATACTCTGCCTTGGTG 294
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Db   241 CAAGGCAAAATGCCACAAATGATGGCAGGTCACAGTTCGTGTAGTATTCTCGCTTTAGTC 300

Qy   295 GCAAGCGGCGCCTTGGATTTGAAGATGCGGTTGCCTTGCTAGCTAAGGCTGGGAGCCTAT 354
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Db   301 TGTGCTGGCGTAATTGATTTTGCTGCTGCGGATTAAACTAGTAGTAGAATTGCGCGGTCAATTA 360

Qy   355 ATGGAAGAAGCGGCTCCTCGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTA 414
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Db   361 ATGCAAGAGAGCTGTACCTGCCGCAAAGTGCGCCCATGTATGCAATTATCGGATTAGATAAT 420

Qy   415 GAGGGTCATTGAAGAGAGCCTGTCAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAAC 474
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Db   421 GATGCTATTGCAAAAGCTGTGAAGAATGGCGGCTCAAGGACAAGTGTCTCACCTGTGAAC 480

Qy   475 TATAACACACCTGCACAAATCGTCATTGCTGAGGAAGTGGTTGCAGTTGATCGAGCGGTT 534
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Db   481 TTTAACTCACCCGGTCAAGTGGTGTATTGGGGTAATAAAGAAGACCGTGCAGGG 540

Qy   535 GAACTTTGCAAGAAGCAGTGCAGTGCCAAACCTTGAGTTCCTCTTAAGGTGTCAGGTCCCTTT 594
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Qy   595 CACACCGCTCTCCTTGAGCCTGCTAGCCAGAAAACTAGCTGAAACTCAGCTCAGGTAAGT 654
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Db    301  GTTTGTTGCTGGGTGTTGGATTTCCAAGATGCGATTAAAATTAGTGGAATTGCGCCGAAAA  360

Qy    352  TATATGGAAGAAGCGGCTCCTTGCTGCCAAGATGGTAGCAGTTCCAATACGCCA  411
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Db    361  TTAATGCACAAGCTGCCTGAAGCGCACTGGCGCAATGTATGCAATCATTGGTTTAGAT  420

Qy    412  GTAGAGGTCATTGAAGAAGCCTGTCAAAAAGCTTCATTGGAGCGTGGTTACTCCAGCC  471
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Db    421  AATGAAGCAATTATTAATGCTGCAACAAGCAGAGGCGAGTCGTCGTATCGTGCGGTGCG  480

Qy    472  AACTATAACACACCTGCACAAATCGTCATTGCTGAGAAGCTTGCTGGTTGATCGAGCG  531
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Qy    532  GTTGAACTTTTGCAAGAAGCAGGTGCAAACGCTGTGATTCCTCTTAAGGTGTCAGGTCCC  591
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Db    541  GCTGCATTATGTGAAAGAAGCAGAGGGGGGCAGAAGCGTGCATTGCCGTGAGCCTACCT  600

Qy    592  TTTCACACCGCTCCTCCTTGAGCCGTGCTAGCCAGAAACTAGCTGAAACTCGAGCTTCAGGT-  650
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Db    661  CAAATTAATACACCAACAATATCGTTATGCTCCAGTATTAAATAACGTTGATGTGAAAGCTGAAACTGAA  720

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Qy    829  GTCTTGTGTCAGGTTTGTTGTTAAAAAAATTG  856
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RESULT 14
US-08-487-429B-1/c
; Sequence 1, Application US/08487429B
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/08/487,429B
; CURRENT FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21

;   NUMBER OF SEQ ID NOS: 1
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO 1
;   LENGTH: 1830121
;   TYPE: DNA
;   ORGANISM: Haemophilus influenzae
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Query Match           21.3%;  Score 196.4;  DB 4;  Length 1830121;
Best Local Similarity 54.1%;  Pred. No. 3.9e-48;
Matches   470;  Conservative    0;  Mismatches  386;  Indels  12;  Gaps   3;

Qy       1 ATGACTAAAACAGCCTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60
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Db  172507 ATGAAAAAATTCGCAATGGTCTTCCCAGGTCAAGGCTCCCAAACTGTCGGTATGCTTGCT 172448

Qy      61 GATTTCTATGATCAGTCATCCGATTGTCAAAGAAACCGATTGATCGAGCGAGTCAGGTGCTC  120
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Db  172447 GATCTTGCAACTGAATATCCAATCGTTATTGAAACATTTAAACAACAGCATCTGATCGCGTT 172388

Qy     121 GGTTATGATTTACGTTATCTCATCGATACGG--AAGAAGACAAACTCAATCAGACCCGC  177
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Db  172387 GGTTATGATTTATGGTATCTTGTTCAACAAGGTCCAGCTGAAGAACTTAATAAAACTTGG 172328

Qy     178 TATACGGAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAG  237
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Db  172327 CAAACTCAGCCGCACTTTAGCTGCTTCAGTCGCTTATTATCGCGTATGCAAGAGAAAAA 172268

Qy     238 GGCTATC------AGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTG  291
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Db  172267 TTTCCTCAATTAAACCAGAGAGTGATGCGCAGTCATCATAGCTTAGGTGAGTCATCTGCGTTA 172208

Qy     292 GTGGCAAGCGGCGCCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTGTGCTAAGCGTGGAGCC  351
           || | | | |  |||| | |||||||  ||||||| || | ||     |  |   |  |
Db  172207 GTTTGTCTGGCGTGTTGGATTTCCAAGATGCGATTAAAATTAGTGGAATTGCGCGAAAA 172148
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Qy      352 TATATGGAAGAGCGGCTCCTGCTGACTCGCAAGATGGTAGCAGTTCTCAATACGCCA 411
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Db   172147 TTAATGCAACAAGCTGTGCCTGAAGGCACTGCGCAATGTATGCAATCATTGGTTTAGAT 172088

Qy      412 GTAGAGGTCATTGAAGAAGCCTGTCAAAAGTTCTGAACTTGGAGTGGTTACTCCAGCC 471
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Db   172087 AATGAAGCAATTATTAATGCTTGCAAACAAGCAGAGAGGAAGCGAAGTCGTATCTGCGGGTG 172028

Qy      472 AACTATAACACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCG 531
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Db   172027 AACTTTAACTCACCGGGTCAAGTAGTTATTGGGGGTCGAAAGCTGCAGTTGAGCGTGCG 171968

Qy      532 GTTGAACTTTGCAAGAAGCAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGTCCC 591
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Db   171967 GCTGCATTATGTAAAGAAGCAGGGGCGAAACGTGCATTGCCGTTAGCTGTGAGCGTACCT 171908

Qy      592 TTTCACACCGCGTCCTCCTGAGCCTGCTAGCCAGAAACTAGCTGAAACTTCTAGCTCAGGT- 650
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Db   171907 TCTCACTGCTGCATTAATGAAACCTGCAGCCGCAATTAGCCGTAACACTTGAGATATATT 171848

Qy      651 --AAGTTTTTCAGATTTTACTTGTCCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAA 708
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Db   171787 GGCACCGAAATTCGTACCGACCTTGTCGTCAGTTATAGTCCAGTTCGTTCGTTGGACTGAA 171728

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RESULT 15
US-10-329-960-1/c
; Sequence 1, Application US/10329960
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
; TITLE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186P1
; CURRENT APPLICATION NUMBER: US/10/329,960
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
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; TYPE: DNA
; ORGANISM: Haemophilus influenzae
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Query Match         21.3%;  Score 196.4;  DB 9;  Length 1830121;
Best Local Similarity  54.1%;  Pred. No. 3.9e-48;
Matches  470;  Conservative   0;  Mismatches 386;  Indels  12;  Gaps  3;

Qy       1 ATGACTAAAACAAGCCTTTTATTTGTTGGTCAAGGTGCCCAGTATCTTAGGGATGGGACGG 60
                                         ||||||||         ||| | | |
Db  172507 ATGAAAAAATTCCAATCGTCTTCCCAGGTCAAGGGTCCCCAAACTGTCGGTATGCTTGCT 172448

Qy      61 GATTCTCATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 120
           ||| ||  |  |||||||||||||       ||       ||    ||  |  |||| ||
Db  172447 GATCTTGCAACTGAATATCCAATCGTTATTGAAACATTTAAACAACAAGCATCGATGCGCTT 172388

Qy     121 GGTTATGATTTACGTTATCCTCATCGATACGG--AAGAAGACAAAACTCAATCAGACCCGC 177
           |||||||||||| ||||||   |||  | |||    |||||  || ||||  |||  |  |
Db  172387 GGTTATGATTTATGGTATCTTGTTCAACAAGGTCCAGCTGAAGAACTAATAAAACTTGG 172328

Qy     178 TATACGCAACCGCCATTCAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAG 237
            |||| |||||||| ||||||| | ||| | |||||   || | |||| ||||||||
Db  172327 CAAACTCAGCCGCGCACTTTTAGCTGCTTCAGTCGCTATTTATCGCGTATGGAAAGAAAAA 172268

Qy     238 GGCTATC------AGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTG 291
           |   |||       |||||| ||| | | |||  | |   |||| || ||  |||| ||
Db  172267 TTTCCTCAATTAAAACCAGAAGTGATGGCAGGTCAGGTCATAGCTTGAGGTATTCTGCCTTA 172208

Qy     292 GTGGCAAGCGGCGGCCCTTGGATTTGAGATGCGGTTGCCTGGTAGCTAAGCGTGAGCC 351
           || | | |  || | ||||||||| |  |||| | || | ||| ||   | | ||| |
Db  172207 GTTTGTGCTGGCGTGTTGGATTTCCAAGATGCCGATTAAATTAGTGGAAATTGCGCGGAAAA 172148

Qy     352 TATATGGAAGAAGCGGCCTCCTGGTGACTCTGCCAAGATGGTAGCAGTTCTCAATACGCCA 411
            |||| |||||||| | |  ||  || |||||| |||||| || ||  | |  |||| |||
Db  172147 TTAATGCAACAAGCTGTGCCTGAAGGCACTGGCGCAATGTATGCAATCATTGGTTTAGAT 172088

Qy     412 GTAGAGGTCATTGAAGAAGCCTGTCAAAAAGCTTCGAACTTGGAGTGGTTACTCCAGCC 471
           | |||  | ||| |||| || ||||||||| | | || ||| | ||  || ||| ||||
Db  172087 AATGAAGCAATTATTAATGCTTGCAAGCAGCAGAGGCCGAAGTCGTATCTGCCGGTG 172028

Qy     472 AACTATAACACACTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTGATCGAGCG 531
           |||| |||| |||| ||  || ||| | ||| |||||||| | | | |||| |||| |
Db  172027 AACTTTAACTCACCGGGTCAAGTAGTTATTGCGGGGTGCGAAAGCTGCAGTGAGCGTGCG 171968

Qy     532 GTTGAACTTTGCAAGAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTCCC 591
           |||||  | ||||||||||| | || | || | || ||| |||| || || |||   ||
Db  171967 GCTGCATTATGTAAAGAAGCAGCGGGGGCAGGGGCGAAAGTGCAATTAGCGGTAACACTTGAGAATATT 171908

Qy     592 TTTCACACGGCTCTCCTTGAGCCTGTAGCCAGAAACTAGCTGAAACTTCTAGCTCAGGT- 650
           |||||| | ||| | |  || |||| || || |   ||||| ||||  ||||   ||||
Db  171907 TCTCACTGTGCATTAATGAAACCTGCACTGCACCGCAGCCAATTAGCGGTAACACTTGAGAATATT 171848

Qy     651 --AAGTTTTCAGATTTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAA 708
             ||  |||||  |||| |  | || | | | |||||| | |||  | | | ||| ||
Db  171847 CAATTAATACACCAACAATATCGGTATTAAAATAACGTTGATGTGAAAACTGAACTGAA 171788
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Qy      709 AAAGAGGACATTGCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAA 768
                |||     |           |  |||||   |  |  |   || |||||||| ||
Db   171787 GGCACCGAAATTCGTACCGCACTTGTGCGTCAGTTATATAGTCCAGTTCGTTGGACTGAA 171728

Qy      769 AGTATTGGGGTCATGCAAGAAGCAGGCATAAGCAACTTATCGAGATTGGACGGGGGAAA 828
            | |||   |||  ||  |||  |   |||||  ||  ||    || ||   ||||||
Db   171727 ACAGTTGAAAAAATGGGCGCAAGATGGCGTTCTAGTGCTTGCTGAAGTGGGGCCAGTAAA 171668

Qy      829 GTCTTGTCAGGTTTGTTAAAAAATTG 856
            ||  ||||   ||||| ||   ||||
Db   171667 GTATTAAATGGTTTAACCAAACCCATTG 171640
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Search completed: June 11, 2003, 19:58:48
Job time : 707 secs

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: June 11, 2003, 20:02:58 ; Search time 233 Seconds
(without alignments)
846.731 Million cell updates/sec

Title: US-09-308-397-2
Perfect score: 1518
Sequence: 1 MTKTAFLFAGGQGAQYLGMGR........QTAHLAHVEDQASLVALLEK 306

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 64473110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata2/paa/PCTUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	1518	100.0	306	17	US-09-308-397-2	Sequence 2, Appli
2	1518	100.0	306	19	US-09-583-110-3912	Sequence 3912, Ap
3	1518	100.0	306	21	US-09-752-069A-143	Sequence 143, App
4	1518	100.0	306	27	US-60-174-089-143	Sequence 143, App
5	1518	100.0	307	15	US-09-107-433-3397	Sequence 3397, Ap
6	1515	99.8	306	1	PCT-US97-22578-171	Sequence 171, App

7	1514	99.7	306	1	PCT-US02-03987-13580	Sequence 13580, A
8	1514	99.7	306	22	US-09-815-242-13580	Sequence 13580, A
9	1514	99.7	306	24	US-10-072-851-13580	Sequence 13580, A
10	1048	69.0	308	27	US-60-360-039-18370	Sequence 18370, Ap
11	948	62.5	328	15	US-09-107-532-6973	Sequence 6973, Ap
12	948	62.5	328	15	US-09-107-532A-6973	Sequence 6973, Ap
13	937	61.7	313	1	PCT-US02-03987-10920	Sequence 10920, A
14	937	61.7	313	22	US-09-815-242-10920	Sequence 10920, A
15	937	61.7	313	24	US-10-072-85-10920	Sequence 10920, Ap
16	937	61.9	315	15	US-09-134-000-4987	Sequence 4987, Ap
17	863	56.9	182	17	US-09-308-397-6	Sequence 6, Appli
18	670	44.1	137	12	US-08-832-030-407	Sequence 407, App
19	669.5	44.1	317	21	US-09-791-537-62681	Sequence 62681, A
20	669.5	44.1	317	27	US-60-360-039-23122	Sequence 23122, A
21	654	43.1	313	27	US-60-360-039-17325	Sequence 17325, A
22	648.5	42.7	333	19	US-09-543-681A-7983	Sequence 7983, Ap
23	646	42.6	306	27	US-60-360-039-19174	Sequence 19174, A
24	646	42.6	313	23	US-09-902-540-14562	Sequence 14562, A
25	643.5	42.4	309	1	PCT-US02-03987-10125	Sequence 10125, A
26	643.5	42.4	309	21	US-09-791-537-94623	Sequence 94623, A
27	643.5	42.4	309	22	US-09-815-242-10125	Sequence 10125, A
28	643.5	42.4	309	24	US-10-072-851-10125	Sequence 10125, A
29	643.5	42.4	309	27	US-60-360-039-793	Sequence 793, App
30	636	41.9	312	1	PCT-US02-03987-10975	Sequence 10975, A
31	636	41.9	312	21	US-09-791-537-28521	Sequence 28521, A
32	636	41.9	312	22	US-09-815-242-10975	Sequence 10975, A
33	636	41.9	312	24	US-10-072-851-10975	Sequence 10975, A
34	632	41.6	318	21	US-09-791-537-6492	Sequence 6492, Ap
35	619	40.8	311	27	US-60-360-039-10002	Sequence 10002, A
36	616.5	40.6	309	21	US-09-791-537-44244	Sequence 44244, A
37	613	40.4	122	17	US-09-308-397-4	Sequence 4, Appli
38	611.5	40.3	307	21	US-09-791-537-122057	Sequence 122057,
39	594.5	39.2	326	21	US-09-791-537-45311	Sequence 45311, A
40	594.5	39.2	326	27	US-60-360-039-62	Sequence 62, Appl
41	594.5	39.2	576775	12	US-08-895-611-2	Sequence 2, Appli
42	594.5	39.2	576775	15	US-09-895-611D-2	Sequence 2, Appli
43	594.5	39.2	576775	18	US-09-458-180-2	Sequence 2, Appli
44	594.5	39.2	576775	22	US-09-895-611D-2	Sequence 2, Appli
45	593	39.1	306	27	US-60-360-039-7062	Sequence 7062, Ap

ALIGNMENTS

RESULT 1
US-09-308-397-2
; Sequence 2, Application US/09308397
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel R.
; APPLICANT: Lonsdale, John T.
; APPLICANT: Payne, David J.
; APPLICANT: Pearson, Stewart C.
; APPLICANT: Van Aller, Glenn
; TITLE OF INVENTION: Novel FabD
; FILE REFERENCE: P50593
; CURRENT APPLICATION NUMBER: US/09/308,397
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: US 60/031,160
; EARLIER FILING DATE: 1996-11-18
; EARLIER APPLICATION NUMBER: PCT/US97/20992
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-308-397-2

Query Match 100.0%; Score 1518; DB 17; Length 306;
Best Local Similarity 100.0%; Pred. No. 6.7e-139;
Matches 306; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY   60
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Db   1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY   60

Qy   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120

Qy 121 EAAPADSGKMVAVLNTPVEVIEEACQKAESELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 EAAPADSGKMVAVLNTPVEVIEEACQKAESELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180

Qy 181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240

Qy 241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300

Qy 301 VALLEK 306
            ||||||
Db 301 VALLEK 306

RESULT 2
US-09-583-110-3912
; Sequence 3912, Application US/09583110
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3912
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3912

Query Match   100.0%; Score 1518; DB 19; Length 306;
Best Local Similarity   100.0%; Pred. No. 6.7e-139;
Matches 306; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY   60
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Db   1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY   60

Qy   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
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Db   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120

Qy 121 EAAPADSGKMVAVLNTPVEVIEEACQKAESELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 EAAPADSGKMVAVLNTPVEVIEEACQKAESELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180

Qy 181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240

Qy 241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300
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Db 241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300

Qy 301 VALLEK 306

Db   301 VALLEK 306
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             301 VALLEK 306

RESULT 3
US-09-752-069A-143
; Sequence 143, Application US/09752069A
; GENERAL INFORMATION:
; APPLICANT: Dougherty, Thomas J.
; APPLICANT: Pucci, Michael J.
; APPLICANT: Dougherty, Brian A.
; APPLICANT: Davison, Daniel B.
; APPLICANT: Bruccoleri, Robert E.
; APPLICANT: Thanassi, Jane A.
; APPLICANT: Farmer II, Bennett T.
; TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
; TITLE OF INVENTION: FOR CELL VIABILITY AND THEIR USES
; FILE REFERENCE: D0001NP
; CURRENT APPLICATION NUMBER: US/09/752,069A
; CURRENT FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/174,089
; PRIOR FILING DATE: 1999-12-30
; SOFTWARE: PatentIn Ver. 2.0
; NUMBER OF SEQ ID NOS: 338
; SEQ ID NO 143
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-752-069A-143

Query Match   100.0%; Score 1518; DB 21; Length 306;
Best Local Similarity   100.0%; Pred. No. 6.7e-139;
Matches 306; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY   60
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Qy   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120

Qy 121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180

Qy 181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240

Qy 241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300

Qy 301 VALLEK 306
            ||||||
Db 301 VALLEK 306

RESULT 4
US-60-174-089-143
; Sequence 143, Application US/60174089
; GENERAL INFORMATION:
; APPLICANT: Dougherty, Thomas J.
; APPLICANT: Pucci Michael J.
; APPLICANT: Dougherty, Brian A.
; APPLICANT: Davidson, Daniel B.
; TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
; TITLE OF INVENTION: FOR CELL VIABILITY AND THEIR USES
; FILE REFERENCE: 30436.44USP1
; CURRENT APPLICATION NUMBER: US/60/174,089
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 226

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 143
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-60-174-089-143

Query Match   100.0%;   Score 1518; DB 27;   Length 306;
Best Local Similarity 100.0%;   Pred. No. 6.7e-139;
Matches 306; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60

Qy   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120

Qy 121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180

Qy 181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240

Qy 241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300

Qy 301 VALLEK 306
         ||||||
Db 301 VALLEK 306

RESULT 5
US-09-107-433-3397
; Sequence 3397, Application US/09107433
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
;   SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
;   THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Dereke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3397:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...307
; SEQUENCE DESCRIPTION: SEQ ID NO: 3397:
US-09-107-433-3397

Query Match   100.0%;   Score 1518; DB 15;   Length 307;
Best Local Similarity 100.0%;   Pred. No. 6.8e-139;
Matches 306; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 61

Qy   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 121

Qy 121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 122 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 181

Qy 181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 182 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 241

Qy 241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 242 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 301

Qy 301 VALLEK 306
         ||||||
Db 302 VALLEK 307

RESULT 6
PCT-US97-22578-171
; Sequence 171, Application PC/TUS9722578
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Burgett, Stanley G.
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Jaskunas Jr., Stanley R.
; APPLICANT: Mills, Bradley J.
; APPLICANT: Norris, Franklin H.
; APPLICANT: Peery, Robert B.
; APPLICANT: Rosteck Jr., Paul R.
; APPLICANT: Skatrud, Paul L.
; APPLICANT: Smith, Michele C.
; APPLICANT: Rockey, Pamela K.
; APPLICANT: Young-Bellido, Michele
; TITLE OF INVENTION: Streptococcus Pneumoniae DNA Sequences
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: U.S.
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```
;   CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: PCT/US97/22578
;      FILING DATE:
;      CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;      NAME: Webster, Thomas D.
;      REGISTRATION NUMBER: 39,872
;      REFERENCE/DOCKET NUMBER: X-11162
;   TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 317-276-3334
;   INFORMATION FOR SEQ ID NO: 171:
;      SEQUENCE CHARACTERISTICS:
;         LENGTH: 306 amino acids
;         TYPE: amino acid
;         STRANDEDNESS: Not Relevant
;         TOPOLOGY: Not Relevant
;      MOLECULE TYPE: peptide
;      HYPOTHETICAL: NO
;      ANTI-SENSE: NO
PCT-US97-22578-171

Query Match           99.8%;  Score 1515;  DB 1;  Length 306;
Best Local Similarity 99.7%;  Pred. No. 1.3e-138;
Matches  305;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60

Qy   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120

Qy  121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180

Qy  181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240
        ||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db  181 LQEAGAKRLIPLKVSGPFH+SLLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240

Qy  241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300

Qy  301 VALLEK 306
        ||||||
Db  301 VALLEK 306


RESULT 7
PCT-US02-03987-13580
; Sequence 13580, Application PC/TUS0203987
; GENERAL INFORMATION:
;   APPLICANT: Elitra Pharmaceuticals, Inc.
;   TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
;   TITLE OF INVENTION: Proliferation
;   FILE REFERENCE: ELITRA.028VPC
;   CURRENT APPLICATION NUMBER: PCT/US02/03987
;   CURRENT FILING DATE: 2002-02-02
;   PRIOR APPLICATION NUMBER: 60/267,636
;   PRIOR FILING DATE: 2001-02-09
;   NUMBER OF SEQ ID NOS: 15811
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13580
;   LENGTH: 306
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
PCT-US02-03987-13580

Query Match           99.7%;  Score 1514;  DB 1;  Length 306;
Best Local Similarity 99.7%;  Pred. No. 1.7e-138;
Matches  305;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;


Qy    1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60

Qy   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120

Qy  121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180

Qy  181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240

Qy  241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300

Qy  301 VALLEK 306
        ||||||
Db  301 VALLEK 306


RESULT 8
US-09-815-242-13580
; Sequence 13580, Application US/09815242
; GENERAL INFORMATION:
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Kari L.
;   APPLICANT: Zyskind, Judith W.
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John D.
;   APPLICANT: Carr, Grant J.
;   APPLICANT: Yamamoto, Robert T.
;   APPLICANT: Xu, H. Howard
;   TITLE OF INVENTION: Identification of Essential Genes in
;   TITLE OF INVENTION: Prokaryotes
;   FILE REFERENCE: ELITRA.011A
;   CURRENT APPLICATION NUMBER: US/09/815,242
;   CURRENT FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: 60/191,078
;   PRIOR FILING DATE: 2000-03-21
;   PRIOR APPLICATION NUMBER: 60/206,848
;   PRIOR FILING DATE: 2000-05-23
;   PRIOR APPLICATION NUMBER: 60/207,727
;   PRIOR FILING DATE: 2000-05-26
;   PRIOR APPLICATION NUMBER: 60/242,578
;   PRIOR FILING DATE: 2000-10-23
;   PRIOR APPLICATION NUMBER: 60/253,625
;   PRIOR FILING DATE: 2000-11-27
;   PRIOR APPLICATION NUMBER: 60/257,931
;   PRIOR FILING DATE: 2000-12-22
;   PRIOR APPLICATION NUMBER: 60/269,308
;   PRIOR FILING DATE: 2001-02-16
;   NUMBER OF SEQ ID NOS: 14110
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13580
;   LENGTH: 306
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae
US-09-815-242-13580

Query Match           99.7%;  Score 1514;  DB 22;  Length 306;
Best Local Similarity 99.7%;  Pred. No. 1.7e-138;
Matches  305;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60
```

```
Qy   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120

Qy  121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180

Qy  181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240

Qy  241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDRTAHLAHVEDQASL 300

Qy  301 VALLEK 306
        ||||||
Db  301 VALLEK 306
```

RESULT 9
US-10-072-851-13580
; Sequence 13580, Application US/10072851
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072,851
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13580
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-072-851-13580

```
Query Match             99.7%;  Score 1514;  DB 24;  Pred. No. 1.7e-138;
Best Local Similarity   99.7%;
Matches   305;  Conservative   1;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1 MTKTAFLFAGGQAGQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MTKTAFLFAGGQAGQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60

Qy   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120

Qy  121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180

Qy  181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240

Qy  241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDRTAHLAHVEDQASL 300

Qy  301 VALLEK 306
        ||||||
Db  301 VALLEK 306
```

RESULT 10
US-60-360-039-18370
; Sequence 18370, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18370
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Lactococcus lactis
US-60-360-039-18370

```
Query Match             69.0%;  Score 1048;  DB 27;  Length 308;
Best Local Similarity   67.5%;  Pred. No. 5.1e-93;
Matches   208;  Conservative   40;  Mismatches   58;  Indels   2;  Gaps   1;

Qy    1 MTKTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60
        |||||||||:||:||:|:::::::||||:|||||||||||||||||||||||||:|:|:|
Db    1 MTKTAFLFSGGQAQKLGMARDLYDQYETVKATFDEASQALGYDLRALIDNDEEKLNETKY 60

Qy   61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
        ||||||:::||||||:||:|:||||||||||||:||||||:||||::::|:||||:|:||
Db   61 TQPAILTTSVAILRLLSENGIKPDLVAGLSLGEYSALVASGIIDFQEAVKLVAKRGQYMT 120

Qy  121 EAAPADSGKMVAVLNTPVEVIEEACQKASEL--GVVTPANYNTPAQIVIAGEVVAVDRAV 178
        |||||:||||||:|||:||:|::|||:|||::  |||||||:||||:||||:|||||||||
Db  121 EAAPTSGKMVAVMNTDPALIEICQKAAEFKGGIVSPANYNTPAQIVIGGEVEAVDYAV 180

Qy  179 ELLQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKE 238
        ||||:||||||||:|||||||||:||||||:||||||||||||||||||:|||:|||||:
Db  181 ELLKEAGVRKLIELKVSGPFHTALLKPASEKLALELDKIDFRPFELPLISNTSAKVMEND 240

Qy  239 DIAQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQA 298
        :::||||||:|:||:||||||::::::||||||||||||:||||||||||||||||||||:
Db  241 EVKGLLTRQVMEPVRFYESVETMQKLGATRFIEVGPGRVLSGFIKKIDKNAEIANVENLA 300

Qy  299 SLVALLEK 306
        ||:  :::
Db  301 SFEALINQ 308
```

RESULT 11
US-09-107-532-6973
; Sequence 6973, Application US/09107532
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7308
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham

```
;         STATE: Massachusetts
;         COUNTRY: USA
;         ZIP: 02354
;    COMPUTER READABLE FORM:
;         MEDIUM TYPE: CD/ROM ISO9660
;         COMPUTER:
;         OPERATING SYSTEM:
;         SOFTWARE:
;    CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: US/09/107,532
;         FILING DATE:
;    PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: 60/ 085598
;         FILING DATE: May 14, 1998
;    PRIOR APPLICATION DATA:
;         APPLICATION NUMBER: 60/051571
;         FILING DATE: July 2, 1997
;    ATTORNEY/AGENT INFORMATION:
;         NAME: Ariniello, Pamela Deneke
;         REGISTRATION NUMBER: 40,489
;         REFERENCE/DOCKET NUMBER: GTC-012
;    TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (781)893-5007
;         TELEFAX: (781)893-8277
; US-09-107-532A-6973:
;    INFORMATION FOR SEQ ID NO: 6973:
;    SEQUENCE CHARACTERISTICS:
;         LENGTH: 328 amino acids
;         TYPE: amino acid
;         TOPOLOGY: linear
;    MOLECULE TYPE: protein
;    HYPOTHETICAL: YES
;    ORIGINAL SOURCE:
;         ORGANISM: Enterococcus faecium
;    FEATURE:
;         NAME/KEY: misc_feature
;         LOCATION: 1...328
US-09-107-532A-6973

Query Match        62.5%;  Score 948;  DB 15;  Length 328;
Best Local Similarity  61.6%;  Pred. No. 3.2e-83;
Matches 188;  Conservative  50;  Mismatches  63;  Indels  4;  Gaps  2;

Qy      3 KTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ 62
          ||||||||||||||||:||||   ::|| : :::|:||||||||||||||||||:|:|||
Db     25 KTAFLFSGGQGAQYQGMGKDLYEE-AVVKQTFDEASEILGYDMAELCFTENERLDQTQYTQ 83

Qy     63 PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA 122
          ||||| ||||||||||:||||||||||||||||:||||||:|||||||||||||||||||
Db     84 PAILTVSIAYYRLLKEHGIIPDAALGLSLGEYSALVASNALSFTEAVALVAKRGAYMTEA 143

Qy    123 APADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ 182
          |||||:| ||:|||||||||::| |:||||:||||||||||||||||:|||:||| ||||
Db    144 TPAGSGKMVAVNNAPIETIEESCHEASKYGIVSPANYNTPQQIVIGGEEKAVDEAVLLLK 203

Qy    183 EAGAKRLIPLKVSGPFHTALLEPASGKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ 242
          ||:|||||||||||||||||||||:|||:  |:|| :|:|||||||||||| ||||||||
Db    204 EKGFKRMIPLNVSGPFHTAILEPAKKLAKDLSQIQFSEPSFPIISNTTTEIMKKETIAG 263

Qy    243 LLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL-- 300
          ||:|:||:| |||||:|:|||||||||||||||||||||||||| ||| ||||:||
Db    264 LLEQQVMQPVRFYESIHKLKTIGIEQVIEVGPGKVLSGFMKKIDKTIPVLRVENKQTFDE 323

Qy    301 -VALL 304
           :|:|
Db    324 TIAIL 328
```

RESULT 12
US-09-107-532A-6973
; Sequence 6973, Application US/09107532A
;   GENERAL INFORMATION:
;   APPLICANT: Lynn A Doucette-Stamm and David Bush
;   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;   STREET: 100 Beaver Street
;   CITY: Waltham
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02354
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: CD/ROM ISO9660
;   COMPUTER: PC
;   OPERATING SYSTEM: <Unknown>
;   SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/107,532A
;   FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 60/ 085,598
;   FILING DATE: 14 May 1998
;   APPLICATION NUMBER: 60/051571
;   FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ariniello, Pamela Deneke
;   REGISTRATION NUMBER: 40,489
;   REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781)893-5007
;   TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6973:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 328 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
;   ORGANISM: Enterococcus faecium
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (B) LOCATION 1...328
; SEQUENCE DESCRIPTION: SEQ ID NO: 6973:
US-09-107-532A-6973

Query Match   62.5%; Score 948; DB 15; Length 328;
Best Local Similarity 61.6%; Pred. No. 3.2e-83;
Matches 188; Conservative 50; Mismatches 63; Indels 4; Gaps 2;

Qy   3 KTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ 62
          ||||||||||||||||:|||| ::|| : :::|:||||||||||||||||||:|:|||
Db   25 KTAFLFSGGQGAQYQGMGKDLYEE-AVVKQTFDEASEILGYDMAELCFTENERLDQTQYTQ 83

Qy   63 PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA 122
          ||||| ||||||||||:||||||||||||||||:||||||:|||||||||||||||||||
Db   84 PAILTVSIAYYRLLKEHGIIPDAALGLSLGEYSALVASNALSFTEAVALVAKRGAYMTEA 143

Qy   123 APADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ 182
          |||||:| ||:|||||||||::| |:||||:||||||||||||||||:|||:||| ||||
Db   144 TPAGSGKMVAVNNAPIETIEESCHEASKYGIVSPANYNTPQQIVIGGEEKAVDEAVLLLK 203

Qy   183 EAGAKRLIPLKVSGPFHTALLEPASGKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ 242
          ||:|||||||||||||||||||||:|||: |:|| :|:|||||||||||| ||||||||
Db   204 EKGFKRMIPLNVSGPFHTAILEPAKKLAKDLSQIQFSEPSFPIISNTTTEIMKKETIAG 263

Qy   243 LLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL-- 300
          ||:|:||:| |||||:|:|||||||||||||||||||||||||| ||| ||||:||
Db   264 LLEQQVMQPVRFYESIHKLKTIGIEQVIEVGPGKVLSGFMKKIDKTIPVLRVENKQTFDE 323

Qy   301 -VALL 304
           :|:|
Db   324 TIAIL 328
```

RESULT 13
PCT-US02-03987-10920
; Sequence 10920, Application PC/TUS0203987
; GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELITRA.028VPC
; CURRENT APPLICATION NUMBER: PCT/US02/03987
; CURRENT FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10920
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
PCT-US02-03987-10920

Query Match             61.7%;   Score 937;   DB 1;   Length 313;
Best Local Similarity   61.9%;   Pred. No. 3.5e-82;
Matches    187;   Conservative    40;   Mismatches    75;   Indels    0;   Gaps    0;

Qy      3  KTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ 62
           ||||||||||||||||||||  ||||:|:::|||||.:|::||||| |:|||||||||||
Db      6  KTAILFSGQGAQYQGMGEELYHQEAIVRETFDEASHILGYEMAELCFTENERLNETEYTQ 65

Qy     63  PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA 122
           |||:|||||:|||||| |||:|||||.||||||||||:||:|||||||||||||||||||
Db     66  PAILTVSVAFYRLLQQKGLTPDVVAGLSLGEYSALVASGALRFSEAVALVQKRGQYMTEA 125

Qy    123  APADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ 182
           ||  ||||||||||||||:||||.|.:|||:||||||||||:||||||||||::||||||
Db    126  APQGTGKMVAVMNAEREVIEKACQEASAFGIVAPANYNTPQQIVIGGEVAAVDQAMTLLK 185

Qy    183  EAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ 242
           ||||||:|||||||||||||:|||.|||:|:||:::||:::|:|||||:||::||||||:
Db    186  EAGVKRMIPLNVSGPFHTALLQPASKKLAQDLAKLNFQTMQIPVISNTTAEIMPQEAIQA 245

Qy    243  LLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASLVA 302
           ||:|:|||||:||||||||||||||||||.|||||:|:|||||||||:|||||||||||:
Db    246  LLEKQVMSAVRFEDSIETMKAMNVGTMIEVGPGKTLTGFVKKIDKTIEMHRVEDVATLTE 305

Qy    303  LL 304
           ||
Db    306  TL 307

RESULT 14
US-09-815-242-10920
; Sequence 10920, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578

---

; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10920
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10920

Query Match             61.7%;   Score 937;   DB 22;   Length 313;
Best Local Similarity   61.9%;   Pred. No. 3.5e-82;
Matches    187;   Conservative    40;   Mismatches    75;   Indels    0;   Gaps    0;

Qy      3  KTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ 62
           ||||||||||||||||||||  ||||:|:::|||||.:|::||||| |:|||||||||||
Db      6  KTAILFSGQGAQYQGMGEELYHQEAIVRETFDEASHILGYEMAELCFTENERLNETEYTQ 65

Qy     63  PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA 122
           |||:|||||:|||||| |||:|||||.||||||||||:||:|||||||||||||||||||
Db     66  PAILTVSVAFYRLLQQKGLTPDVVAGLSLGEYSALVASGALRFSEAVALVQKRGQYMTEA 125

Qy    123  APADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ 182
           ||  ||||||||||||||:||||.|.:|||:||||||||||:||||||||||::||||||
Db    126  APQGTGKMVAVMNAEREVIEKACQEASAFGIVAPANYNTPQQIVIGGEVAAVDQAMTLLK 185

Qy    183  EAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ 242
           ||||||:|||||||||||||:|||.|||:|:||:::||:::|:|||||:||::||||||:
Db    186  EAGVKRMIPLNVSGPFHTALLQPASKKLAQDLAKLNFQTMQIPVISNTTAEIMPQEAIQA 245

Qy    243  LLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASLVA 302
           ||:|:|||||:||||||||||||||||||.|||||:|:|||||||||:|||||||||||:
Db    246  LLEKQVMSAVRFEDSIETMKAMNVGTMIEVGPGKTLTGFVKKIDKTIEMHRVEDVATLTE 305

Qy    303  LL 304
           ||
Db    306  TL 307

RESULT 15
US-10-072-851-10920
; Sequence 10920, Application US/10072851
; GENERAL INFORMATION:
; APPLICANT: Carr, Grant J.
; APPLICANT: Xu, H. Howard
; APPLICANT: Foulkes, J. Gordon
; APPLICANT: Zamudio, Carlos
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072,851
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10920
; LENGTH: 313

```
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-10-072-851-10920

Query Match          61.7%;   Score 937;  DB 24;  Length 313;
Best Local Similarity  61.9%;   Pred. No. 3.5e-82;
Matches 187;  Conservative 40;  Mismatches 75;  Indels  0;  Gaps  0;

Qy    3  KTAPLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEBDKLNQTRYTQ  62
         ||||:|:||||||||::|||:||:|:|| ||| :| :::||:|:|:||:|||:|| ||||
Db    6  KTAILFSGGQAQYQGMGEELYHQEAIVRETFDEASHIIGYEMAELCFTENERLNETEYTQ  65

Qy   63  PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA  122
         ||||:|||| |||||:: ||:|||||||||||||||||:|:||||||:|||:|||||||
Db   66  PAILTVSVAFYRLLQQKGLTPDVVAGLSLGEYSALVASGALRFSEAVALVQKRGQYMTEA  125

Qy  123  APADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ  182
         ||:::||||:|::||||||| |:: |:|:|||:||||||||||||||:||:|:||||| |:
Db  126  APQGTGKMVAVMNAEREVIEKACQEASAFGIVAPANYNTPQQIVIGGEVAAVDQAMTLLK  185

Qy  183  EAGAKRLIPLKVSGPFHTALLBPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ  242
         |||| |||| |||||||||||:||||||||:| |:|::: |||| :||| :||:||:||
Db  186  EAGVKRMIPLNVSGPFHTALLQPASKKLAQDLAKLNFQTMQIPVISNTTAEIMPQEAIQA  245

Qy  243  LLTRQVKEPVRFYESIGVWQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASLVA  302
         ||| || || ||:||| :|||| ||| ||||||| ||| || | |:::||:||||:|:||
Db  246  LLEKQVMSAVRFEDSIETMKAMNVGTMIEVGPGKTLTGFVKKIDKTIEMHRVEDVATLTE  305

Qy  303  LL  304
         ||
Db  306  TL  307
```

Search completed: June 11, 2003, 20:10:43
Job time : 236 secs

```
                     GenCore version 5.1.6
           Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - protein search, using sw model

Run on:    June 11, 2003, 20:03:47 ; Search time 80 Seconds
                                     (without alignments)
                                     867.756 Million cell updates/sec

Title:          US-09-308-397-2
Perfect score:  1518
Sequence:       1 MTKTAFLFAGGQGAQYLGMGR........QTAHLAHVEDQASLVALLEK 306

Scoring table:  BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:       1050967 seqs, 22684292 residues

Total number of hits satisfying chosen parameters:   1050967

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Pending_Patents_AA_New:*
             1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
             2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
             3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
             4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
             5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
             6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
             7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

                                SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1515	99.8	306	6	US-10-282-122A-73805	Sequence 73805, A
2	1108	73.0	306	6	US-10-282-122A-72188	Sequence 72188, A
3	1048	69.0	308	6	US-10-369-493-18370	Sequence 18370, A
4	1036	68.0	312	6	US-10-282-122A-74709	Sequence 74709, A
5	952	62.7	305	6	US-10-282-122A-57675	Sequence 57675, A
6	948	62.5	328	6	US-10-417-884-6973	Sequence 6973, A
7	937	61.7	309	6	US-10-282-122A-56896	Sequence 56896, A
8	937	61.7	315	5	US-09-134-000C-4987	Sequence 4987, Ap
9	937	61.7	315	6	US-09-134-000C-4987	Sequence 4987, Ap
10	937	61.7	315	6	US-10-434-665-4987	Sequence 4987, Ap
11	713.5	47.0	308	6	US-10-282-122A-52133	Sequence 52133, A
12	669.5	44.1	317	6	US-10-369-493-23122	Sequence 23122, A
13	657.5	43.3	312	6	US-10-282-122A-77375	Sequence 77375, A
14	654	43.1	313	6	US-10-369-493-17325	Sequence 17325, A
15	649.5	42.8	310	6	US-10-282-122A-68370	Sequence 68370, A
16	647	42.6	318	6	US-10-282-122A-52405	Sequence 52405, A
17	646	42.6	306	6	US-10-369-493-19174	Sequence 19174, A
18	643.5	42.4	309	6	US-10-282-122A-56519	Sequence 56519, A
19	643.5	42.4	309	6	US-10-369-493-793	Sequence 793, App
20	636	41.9	312	6	US-10-282-122A-58091	Sequence 58091, A
21	628.5	41.4	309	6	US-10-282-122A-78414	Sequence 78414, A
22	626	41.2	312	6	US-10-282-122A-67441	Sequence 67441, A
23	625.5	41.2	308	6	US-10-282-122A-59351	Sequence 59351, A
24	619	40.8	311	6	US-10-369-493-10002	Sequence 10002, A
25	616.5	40.6	309	6	US-10-282-122A-75151	Sequence 75151, A
26	612.5	40.3	309	6	US-10-282-122A-75888	Sequence 75888, A
27	610	40.2	315	6	US-10-282-122A-61523	Sequence 61523, A
28	602.5	39.7	364	6	US-10-282-122A-67853	Sequence 67853, A
29	598	39.4	308	6	US-10-282-122A-72822	Sequence 72822, A
30	594.5	39.2	326	6	US-10-369-493-62	Sequence 62, Appl
31	593	39.1	306	6	US-10-369-493-7062	Sequence 7062, Ap
32	593	39.1	311	6	US-10-282-122A-49082	Sequence 49082, A
33	590	38.9	310	6	US-10-282-122A-49967	Sequence 49967, A
34	588.5	38.8	313	6	US-10-282-122A-60662	Sequence 60662, A
35	584	38.5	306	6	US-10-369-493-8524	Sequence 8524, Ap
36	582.5	38.4	314	6	US-10-282-122A-46082	Sequence 46082, Ap
37	582	38.3	297	6	US-10-369-493-4306	Sequence 4306, Ap
38	580.5	38.2	302	6	US-10-369-493-13673	Sequence 13673, A
39	580	38.2	322	6	US-10-282-122A-47505	Sequence 47505, A
40	570	37.5	308	6	US-10-282-122A-65737	Sequence 65737, A
41	569.5	37.5	307	6	US-10-369-493-15988	Sequence 15988, A
42	569.5	37.5	312	6	US-10-369-493-15613	Sequence 15613, A
43	568.5	37.5	306	6	US-10-369-493-16346	Sequence 16346, A
44	568	37.4	295	6	US-10-282-122A-48856	Sequence 48856, A
45	556.5	36.7	312	6	US-10-282-122A-66433	Sequence 66433, A

                                ALIGNMENTS

```
RESULT 1
US-10-282-122A-73805
; Sequence 73805, Application US/10282122A
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT: Zamudio, Carlos
;  APPLICANT: Malone, Cheryl
;  APPLICANT: Haselbeck, Robert
;  APPLICANT: Ohlsen, Karl
;  APPLICANT: Zyskind, Judith
;  APPLICANT: Wall, Daniel
;  APPLICANT: Trawick, John
;  APPLICANT: Carr, Grant
;  APPLICANT: Yamamoto, Robert
;  APPLICANT: Forsyth, R.
;  APPLICANT: Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-02-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 73805
;  LENGTH: 306
;  TYPE: PRT
;  ORGANISM: Streptococcus pneumoniae
US-10-282-122A-73805
```

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Query Match          99.8%;  Score 1515;  DB 6;  Length 306;
Best Local Similarity 99.7%;  Pred. No. 4.8e-124;
Matches  305;  Conservative  1;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MTKTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MTKTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY   60

Qy   61  TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME  120

Qy  121  EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL  180

Qy  181  LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI  240

Qy  241  AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL  300

Qy  301  VALLEK  306
         ||||||
Db  301  VALLEK  306
```

RESULT 2
US-10-282-122A-72188
; Sequence 72188, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 72188

; LENGTH: 306
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-282-122A-72188

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Query Match          73.0%;  Score 1108;  DB 6;  Length 306;
Best Local Similarity 71.8%;  Pred. No. 1.7e-88;
Matches  219;  Conservative  37;  Mismatches  49;  Indels  0;  Gaps  0;

Qy    1  MTKTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY   60
         |||||||||||||||:||| . :: . : . ::||| . ||||:|. ||.||||||||||
Db    1  MTKTAFLFAGGQAQKLGMASDLYEIYPVVKETFKTAHSILGYDVRALIDNDEEKLNQTRY   60

Qy   61  TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME  120
         :|||||:|||||||||:|||||||:|||||||||||||:||||:|||||:||||||.|:||
Db   61  AQPAILTTSVAIYRLLKEKGYQPDIVAGLSLGEYSALVAAGAISFEDALALVAKRGEFME  120

Qy  121  EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL  180
         .|||| . |||||:||.  :||||.||||:. |:|:||||||||:||:|||| .|||:||||
Db  121  TAAPAGVGKMVAVMNTDPRLIEEICQKASSKGIVSPANYNTPTQIVIGGEVAAVDYAVEL  180

Qy  181  LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI  240
         |: .|.|||:.|||||||||||:.||||||| . ||:.||. :|:|:||||||.. :|:|:.
Db  181  LKGAGSKRLISLKVSGPFHTALLKSASQKLAQALENIKFSDFMLPLVGNTKAEIMKEQEI  240

Qy  241  AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL  300
         . ||:|||||||||||||.|||: . | . ||:|||||||||||||:.||:.||||:||||
Db  241  KPLLARQVKEPVRFYESIAVMQKFGVNNYVEIGPGKVLSGFVKKIDKSAKISAVEDLASL  300

Qy  301  VALLE  305
         |.:|:
Db  301  QAFLD  305
```

RESULT 3
US-10-369-493-18370
; Sequence 18370, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18370
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Lactococcus lactis
US-10-369-493-18370

```
Query Match          69.0%;  Score 1048;  DB 6;  Length 308;
Best Local Similarity 67.5%;  Pred. No. 3e-83;
Matches  208;  Conservative  40;  Mismatches  58;  Indels  2;  Gaps  1;

Qy    1  MTKTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY   60
         ||||||||.|||||:|||.:||||||| . : . ||||:| .||||||:||||||||:||:|
Db    1  MTKTAFLFSGGQAQKLGMAARDLYDQYETVXATFDEASQALGYDLRLALIDNDEEKLNETKY   60

Qy   61  TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME  120
         ||||||:||||||||:|::|:||||:||||||||||||||||::||:||:|||||||.|||:
Db   61  TQPAILTTSVAILRLLSENGIKPDLVAGLSLGEYSALVASGIIDFQEAVKLVAKRGQYMT  120

Qy  121  EAAPADSGKMVAVLNTPVEVIEEACQKASEL--GVVTPANYNTPAQIVIAGEVVAVDRAV  178
         ||||. . |||||:||. :||||.|||: . | . |||:||||||||:||.|||| . |:||
Db  121  EAAPTGSGKMVAVMNTDPALIEEICQKAAEFKGGIVSPANYNTPAQIVIGGEVEAVDYAV  180
```

```
Qy  121 EAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVEL 180
        ||||  |||||||  ||| ||:||| |::||| ||| ||||||| |||: |: ||| |||
Db  121 EAAPQGSGKMVAVMNTDVQVIEEVCQIAKHGVVAPANYNTPSQIVIGGQTDAVNVAVEL 180

Qy  181 LQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDI 240
        | : ||||||| ||||||||||||||: || :| ||: ::|||| ||||||||| |:||
Db  181 LKERGVKRLIPLNVSGPFHTALLEPASRLLAKELERYNFSDFKIPLVGNTEANIMEKDRI 240

Qy  241 AQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVVKKIDQTAHLAHVEDQASL 300
         :||:||| :||||| :: ::| || ||:|||||||| ||||:|||| :: | :: ||:|
Db  241 PELLARQVMEPVRFYDSVATLVESGITQFIEVGPGKVLTGFVKKIDKNLLCTSVENMVSL 300

Qy  301 VALLEK 306
          |:::
Db  301 RLFLDR 306
```

```
RESULT 5
US-10-282-122A-57675
; Sequence 57675, Application US/10282122A
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT: Zamudio, Carlos
;  APPLICANT: Malone, Cheryl
;  APPLICANT: Haselbeck, Robert
;  APPLICANT: Ohlsen, Kari
;  APPLICANT: Zyskind, Judith
;  APPLICANT: Wall, Daniel
;  APPLICANT: Trawick, John
;  APPLICANT: Carr, Grant
;  APPLICANT: Yamamoto, Robert
;  APPLICANT: Forsyth, R.
;  APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57675
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57675

Query Match       62.7%;  Score 952;  DB 6;  Length 305;
Best Local Similarity  62.0%;  Pred. No. 7.2e-75;
Matches 189;  Conservative 50;  Mismatches 62;  Indels 4;  Gaps 2;

Qy  3 KTAPLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ 62
```

```
Qy  179 ELLQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKE 238
        |||:||| :|||| ||||||||:| ||||: || :| :::| :|| ||:||||:|| |:
Db  181 ELLKEAGVRKLIELKVSGPFHTAILKPASKLALELDKIDFRPFELPLISNTSAKVMEND 240

Qy  239 DIAQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVVKKIDQTAHLAHVEDQA 298
        : ||:||||| :||||||| :|:|| ||:| |||||||:||||| |:||| :: | :: :|
Db  241 EVKGLLTRQVMEPVRFYESVETMQKLGATRFIEVGPGRVLSGFIKKIDKNAEIANVENLA 300

Qy  299 SVVALLEK 306
          |: :|
Db  301 SFEALINQ 308
```

```
RESULT 4
US-10-282-122A-74709
; Sequence 74709, Application US/10282122A
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT: Zamudio, Carlos
;  APPLICANT: Malone, Cheryl
;  APPLICANT: Haselbeck, Robert
;  APPLICANT: Ohlsen, Kari
;  APPLICANT: Zyskind, Judith
;  APPLICANT: Wall, Daniel
;  APPLICANT: Trawick, John
;  APPLICANT: Carr, Grant
;  APPLICANT: Yamamoto, Robert
;  APPLICANT: Forsyth, R.
;  APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
US-10-282-122A-74709
; SEQ ID NO 74709
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74709

Query Match       68.2%;  Score 1036;  DB 6;  Length 312;
Best Local Similarity  68.3%;  Pred. No. 3.4e-82;
Matches 209;  Conservative 39;  Mismatches 58;  Indels 0;  Gaps 0;

Qy  1 MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRY 60
        |||||||||||||| ||| ||||| | || :|| |||||||||||||| |:::|||||| |
Db  1 MTKTAFLFAGQGAQKLGMARDFYDNPAIVRKTFDQASQVLGYDLRRLIDSDELKLNQTSY 60

Qy  61 TQPAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYME 120
        |||||| :|:|||| | : | |||||||||||||||||||||| |||:: |||||||  ||
Db  61 TQPAILTSSIAIYRVLGLHHVKPDMVAGLSLGEYSALVASGALSFEDTLSLVAKRGRLME 120
```

US-10-417-884-6973

```
Query Match             62.5%;  Score 948;  DB 6;  Length 328;
Best Local Similarity   61.6%;  Pred. No. 1.8e-74;
Matches 188;  Conservative  50;  Mismatches  63;  Indels  4;  Gaps  2;

Qy     3  KTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ   62
          ||||||:||||:||:.|::| |:.|: :||:  :|||: :|: ::|:||:::|:||:||||
Db    25  KTAFLFSGQGAQYQGMGKDLYEE-AVVKQTFDEASEILGYDMAELCFTENERLDQTQYTQ   83

Qy    63  PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA  122
          ||||:.|||||||:||||| || |||||||||||||:| |:.|| |:|||||||||||  
Db    84  PAILTVSIAYYRLLKEHGIIPDAALGLSLGEYSALVASNALSFTEAVALVAKRGAYMTEA  143

Qy   123  APADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ  182
          ||| |||||| :: ||||||: .|: ||||| |||||||||:|| |: |::|: ::||||
Db   144  TPAGSGKMVAVMNAPIETIEESCHEASKYGIVSPANYNTPQQIVIGGEEKAVDEAVLLLK  203

Qy   183  EAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ  242
          |::.||:|.|||:||||||||||:.|: |:::|::|:  |||:|.:|:|||: :|.| :.
Db   204  EKGFKRMIPLNVSGPFHTAILEPAAKLAKDLSQIQFSEPSFPIISNTTEIMKKETIAG-  263

Qy   243  LLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL--  300
          ||:::| :||||||||.|| |: |.|:.|::| |||||| ||||||:|: |:||::||
Db   264  LLEQQVMQPVRFYESIHKLKTIGIEQVIEVGPGKVLSGFMKKIDKTIPVLRVENKQTFDE  323

Qy   301  -VALL  304
           :||
Db   324  TIAIL  328
```

RESULT 6

US-10-417-884-6973
; Sequence 6973, Application US/10417884
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;   ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;   STREET: 100 Beaver Street
;   CITY: Waltham
;   STATE: Massachusetts
;   COUNTRY: USA
;   ZIP: 02354
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: CD/ROM ISO9660
;   COMPUTER: PC
;   OPERATING SYSTEM: <Unknown>
;   SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/417,884
;   FILING DATE: 17-Apr-2003
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/09/107,532A
;   FILING DATE: 30-Jun-1998
;   APPLICATION NUMBER: 60/085,598
;   FILING DATE: 14 May 1998
;   APPLICATION NUMBER: 60/051571
;   FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ariniello, Pamela Deneke
;   REGISTRATION NUMBER: 40,489
;   REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (781)893-5007
;   TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 6973:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 328 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;   ORGANISM: Enterococcus faecium
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (B) LOCATION 1...328
; SEQUENCE DESCRIPTION: SEQ ID NO: 6973:
```
 Db     2  KTAFLFSGQGAQYQGMGKDLYEE-AVVKQTFDEASEILGYDMAELCFTENERLDQTQYTQ   60

 Qy    63  PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA  122
           ||||:.|||||||:||||| || |||||||||||||:| |:.|| |:||||||||||
 Db    61  PAILTVSIAYYRLLKEHGIIPDAALGLSLGEYSALVASNALSFTEAVALVAKRGAYMTEA  120

 Qy   123  APADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ  182
           ||| |||||| :: ||||||: .|: ||||| |||||||||:|| |: |::|: ::||||
 Db   121  APAGSGKMVAVMNAPIETIEESCHEASKYGIVSPANYNTPQQIVIGGEEKAVDEAVLLLK  180

 Qy   183  EAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ  242
           |::.||:|.|||:||||||||||:.|: |:::|::|:  |||:|.:|:|||: :|.| :.
 Db   181  EKGFKRMIPLNVSGPFHTAILEPAAKLAKDLSQIQFSEPSFPIISNTTEIMKKETIAG-  240

 Qy   243  LLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASL--  300
           ||:::| :||||||||.|| |: |.|:.|::| |||||| ||||||:|: |:||::||
 Db   241  LLEQQVMQPVRFYESIHKLKTIGIEQVIEVGPGKVLSGFMKKIDKTIPVLRVENKQTFDE  300

 Qy   301  -VALL  304
            :||
 Db   301  TIAIL  305
```

RESULT 7

US-10-282-122A-56896
; Sequence 56896, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56896
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-282-122A-56896

Query Match    61.7%;  Score 937;  DB 6;  Length 309;
Best Local Similarity   61.9%;  Pred. No. 1.5e-73;
Matches 187;  Conservative 40;  Mismatches 75;  Indels 0;  Gaps 0;

Qy    3  KTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ  62
         || |:||||||||  |||::|  |::||  |::|| | :|:|:|  ::| :|:|
Db    2  KTAILFSGGQAQYQGMGEELYHQEAIVRETFDEASHILGYEMAELCFTENERLNETEYTQ  61

Qy   63  PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA 122
         ||||  || ||||||:|| ||:|||||||||||||||||||| | : ||||| |||:||: 
Db   62  PAILTVSVAFYRLLQQKGLTPDVVAGLSLGEYSALVASGALRFSEAVALVQKRGQYMTEA 121

Qy  123  APADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ 182
         ||  :||||||:| |:||:||| |:||::|:| |||||||| :|||:||| ||:| :||: 
Db  122  APQGTGKMVAVMNAEREVIEKACQEASAFGIVAPANYNTPQQIVIGGEVAAVDQAMTLLK 181

Qy  183  EAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ 242
         ||| ||:|||:|||||||| |||::|||::|| : |:  | ||||||| |||: |:| |: 
Db  182  EAGVKRMIPLNVSGPFHTALLQPASKKLAQDLAKLNFQTMQIPVISNTTAEIMPQEAIQA 241

Qy  243  LLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASLVA 302
         ||  ||  |||| | | |:|   | :||||||| |||| ||||||:|  |  ||| ::|  
Db  242  LLEKQVMSAVRFEDSIETMKAMNVGTMIEVGPGKTLTGFVKKIDKTIEMHRVEDVATLTE 301

Qy  303  LL 304
         ||
Db  302  TL 303

RESULT 8
US-09-134-000C-4987
; Sequence 4987, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4987
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4987

Query Match    61.7%;  Score 937;  DB 5;  Length 315;
Best Local Similarity   61.9%;  Pred. No. 1.5e-73;
Matches 187;  Conservative 40;  Mismatches 75;  Indels 0;  Gaps 0;

Qy    3  KTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ  62
         || |:||||||  |||::|  |::||  |::|| | :|:|:|  ::| :|:|
Db    8  KTAILFSGGQAQYQGMGEELYHQEAIVRETFDEASHILGYEMAELCFTENERLNETEYTQ  67

Qy   63  PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA 122
         ||||  || ||||||:|| ||:|||||||||||||||||||
Db   68  PAILTVSVAFYRLLQQKGLTPDVVAGLSLGEYSALVASGALRFSEAVALVQKRGQYMTEA 127

Qy  123  APADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ 182
         ||  :||||||:| |:||:||| |:||::|:| |||||||
Db  128  APQGTGKMVAVMNAEREVIEKACQEASAFGIVAPANYNTPQQIVIGGEVAAVDQAMTLLK 187

Qy  183  EAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ 242
```

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Db  188  EAGVKRMIPLNVSGPFHTALLQPASKKLAQDLAKLNFQTMQIPVISNTTAEIMPQEAIQA 247

Qy  243  LLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASLVA 302
         ||  ||  |||| | | |:|   | :||||||| |||| ||||||:|  |  ||| ::|  
Db  248  LLEKQVMSAVRFEDSIETMKAMNVGTMIEVGPGKTLTGFVKKIDKTIEMHRVEDVATLTE 307

Qy  303  LL 304
         ||
Db  308  TL 309

RESULT 9
US-09-134-000C-4987
; Sequence 4987, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4987
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4987

Query Match    61.7%;  Score 937;  DB 5;  Length 315;
Best Local Similarity   61.9%;  Pred. No. 1.5e-73;
Matches 187;  Conservative 40;  Mismatches 75;  Indels 0;  Gaps 0;

Qy    3  KTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEDKLNQTRYTQ  62
         || |:||||||  |||::|  |::||  |::|| | :|:|:|  ::| :|:|
Db    8  KTAILFSGGQAQYQGMGEELYHQEAIVRETFDEASHILGYEMAELCFTENERLNETEYTQ  67

Qy   63  PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA 122
         ||||  || ||||||:|| ||:|||||||||||||||||||
Db   68  PAILTVSVAFYRLLQQKGLTPDVVAGLSLGEYSALVASGALRFSEAVALVQKRGQYMTEA 127

Qy  123  APADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ 182
         ||  :||||||:| |:||:||| |:||::|:| |||||||
Db  128  APQGTGKMVAVMNAEREVIEKACQEASAFGIVAPANYNTPQQIVIGGEVAAVDQAMTLLK 187

Qy  183  EAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ 242
         ||| ||:|||:|||||||| |||::|||::|| : |:  | ||||||| |||: |:| |: 
Db  188  EAGVKRMIPLNVSGPFHTALLQPASKKLAQDLAKLNFQTMQIPVISNTTAEIMPQEAIQA 247

Qy  243  LLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASLVA 302
         ||  ||  |||| | | |:|   | :||||||| |||| ||||||:|  |  ||| ::|  
Db  248  LLEKQVMSAVRFEDSIETMKAMNVGTMIEVGPGKTLTGFVKKIDKTIEMHRVEDVATLTE 307

Qy  303  LL 304
         ||
Db  308  TL 309

RESULT 10
US-10-434-665-4987
; Sequence 4987, Application US/10434665
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-09
; CURRENT APPLICATION NUMBER: US/10/434,665
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 09/134,000
; PRIOR FILING DATE: 1998-08-13
```

; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4987
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-434-665-4987

Query Match   61.7%;   Score 937;   DB 6;   Length 315;
Best Local Similarity   61.9%;   Pred. No. 1.5e-73;
Matches 187;   Conservative 40;   Mismatches 75;   Indels 0;   Gaps 0;

```
Qy    3 KTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLIDTEEBDKLNQTRYTQ 62
          ||:||||||||||||||||||||||||||||||||||||||||||:::
Db    8 KTAILFSGGQAQYQGMGEELYHQBAIVRETFDEASHILGYEMAELCFFTENERLNETEYTQ 67

Qy   63 PAILATSVAIYRLLQEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAYMEEA 122
          ||::||||||||||||||||||||||||||||||||||||||||||||:
Db   68 PAILTVSVAFYRLLQQKGLTPDVVAGLSLGEYSALVASGALRFSEAVALVQKRGQYMTEA 127

Qy  123 APADSGKMVAVLNTPVEVIEBACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAVELLQ 182
          :||||||::||||||||||||||||||||||||||||||
Db  128 APQGTGKMVAVMNAEREVIEKACQEASAFGIVAPANYNTPQQIVIGGEVAAVDQAMTLLK 187

Qy  183 EAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGNTEAAVMQKEDIAQ 242
          |||||||||||||||||||||||||||||||||:  ::  :
Db  188 EAGVKRMIPLNVSGPFHTALLQPASKKLAQDLAKLNFQTMQIPVISNTTAEIMPQEAIQA 247

Qy  243 LLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQASLVA 302
          :||||||||||||||||||:  |  :|:||::|||:
Db  248 LLEKQVMSAVRFEDSIETMKAMNVGTMIEVGPGKTLTGFVKKIDKTIEMHRVEDVATLTE 307

Qy  303 LL 304
         ||
Db  308 TL 309
```

RESULT 11
US-10-282-122A-52133
; Sequence 52133, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52133
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-52133

Query Match   47.0%;   Score 713.5;   DB 6;   Length 308;
Best Local Similarity   48.5%;   Pred. No. 4.9e-54;
Matches 147;   Conservative 56;   Mismatches 97;   Indels 3;   Gaps 3;

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Qy    1 MTKTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYL-IDTEEDKLNQTR 59
          ||||||||||||||||||||||:  :|::|:::|||: ::
Db    1 MGKIAFVFSGGQSQYVGMGKDLYDNYQSAKETFDKADEVLGFKISELCFEGKDEELNLTE 60

Qy   60 YTQPAILATSVAIYRLL-QEKGYQPDMVAGLSLGEYSALVASGALDFEDAVALVAKRGAY 118
          |||  |:|: ||||||  :|||||||||||||||||||||||::
Db   61 NTQPAVLITSIAALRALEEEKGIKPDVVAGLSLGEYSAHVCSGSFEDAVRLVKKRGRY 120

Qy  119 MEEAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAV 178
          |:  :  ::||||||||||||||||  :||||
Db  121 MQBAVPKGIGTMAAIIGLEGDVVRGICAEQSKEGIVEVANYNCPGQIVIAGEVKAVESAC 180

Qy  179 ELLQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVSFSDFTCPLVGN-TEAAVMQK 237
          ||||||||||||||||||||||::   :||::|::||::::::
Db  181 TKLKESGARRTVMLSVSGPFHTSMLKSAAEKLEEELKNINIEDMKVPVITNVTGDYVEDK 240

Qy  238 EDIAQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQ 297
          |:|||||::||::|:
Db  241 DQIKGLLKKQVMSSVRWEDTIRRMMDDGVDTFIELGPGKTLSSFIKKINRKMTIFNIEKA 300

Qy  298 ASL 300
Db  301 EDL 303
```

RESULT 12
US-10-369-493-23122
; Sequence 23122, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23122
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23122

Query Match   44.1%;   Score 669.5;   DB 6;   Length 317;
Best Local Similarity   47.2%;   Pred. No. 3.6e-50;
Matches 143;   Conservative 47;   Mismatches 110;   Indels 3;   Gaps 3;

```
Qy    1 MTKTAFLFAGGQAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLI-DTEEDKLNQTR 59
          ||| ||||||  |||::||||  |:  |  :|   :|||:
```

```
Best Local Similarity  47.4%;  Pred. No. 3.9e-49;
Matches 146;  Conservative 58;  Mismatches 97;  Indels 7;  Gaps 4;

Qy    1  MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDLRYLI-DTEEDKLNQTR   59
         |||| |||  ||| ::| ||  :|  |:|||| :::|:|::|||| ||:||: ||||||||:::
Db    6  MSKFAIVFPGQGSQAVGMLADLABQYAVVKQTFAEASEVLGYDLWALVQDGPVEDLNQTF   65

Qy   60  YTQPAILATSVAIYRLLQEKGY-QPDMVAGLSGEYSALVASGALDFEDAVALVAKRGAY   118
         :|||| |:::|| :|  |:: |  |:|| ||:|||||||: |:| |:|| | |  ||||
Db   66  RTQPALLAASVAINRVWQQLGLEQPAVLAGHSLGEYSALVCAGVIDFKQAIKLVELRGQL  125

Qy  119  MEEAAPADSGKMVAVLNTPVEVIEEACQKASELGVVTPANYNTPAQIVIAGEVVAVDRAV  178
         |  | |  :|  :|  |   ||: :||::| ||| :| :||:| |||||||  |:|
Db  126  MQQAVPAGTGAMYAIIGLEDEAIAXACADAAQGEVVSPVNFNSPGQVVIAGQKDAVERAG  185

Qy  179  ELLQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVFSDFTCPLVGNTEAAVMQKE   238
         : |:||||| ||| |:||:||::||  |:|||| |||:||  |     |||| ||| ||
Db  186  VLCKEAGAKRALPLPVSVPSHCALMKPAADELAKTLAELEFNAPQIPVINNVD--VVAET  243

Qy  239  D--IAQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVE   295
         |  :|:|| ||: ||||| | : ||::||  :||:|||||||:|: |:| ||||||||:|
Db  244  DPVKIKDALIRQLYSPVRWTECVEQMSAQGVEKLIEMGPGKVLTGLTKRIVKTLEGVAVN  303

Qy  296  DQASLVAL  303
         | ||| ||
Db  304  DVASLDAV  311
```

```
Db    1  MSKIAFLFPGQGSQFIGMGKELYEQVPAAKRLFDEADETLETKLSSLIFEGDAEELTLTY   60
         |||:|:|||||||| :||| | || : |:||||:| : ||||:|:|  ||| : :|:|:|
Qy   60  YTQPAILATSVAIYRLLQEKGYQPDMVAGLSGEYSALVASGALDFEDAVALVAKRGAYM   119
Db   61  NAQPALLTTSIAVLEKPKESGITPDFTAGHSLGEYSALVAAGALSFKDAVVTVKRGEFM   120
Qy  120  EEAAPADSGKMVAVLNTPVEVIEEACQKASELG-VVTPANYNTPAQIVIAGEVVAVDRAV  178
         | |  |  :|::|  |    |:  |::: : :  :|  | |:  :|||:||  |:||
Db  121  NEAVPAGEGAMAAILGMDAEALKQVTDKVTEEGNLVQLANLNCPGQIVISGTAKGVELAS  180
Qy  179  ELLQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVFSDFTCPLVGNTEAAVM-QK   237
         | :||||| || | ::|||||: |:||||: :|| || :  |    |:|   | :| :|
Db  181  ELAKENGAKRAIPLEVSGPFHSELMKPAAEKLKEVLDACDIKDADVPVISNVSADVMTEK  240
Qy  238  EDIAQLLTRQVKEPVRFYESIGVMQEAGISNFIEIGPGKVLSGFVKKIDQTAHLAHVEDQ  297
         .||::| :||:| ||||:|| ::::||| : |||||||||||:|||:::  |:  :| ||:|
Db  241  ADIKEKLIEQLYSPVRFEESINKLIAEGVTTFIEIGPGKVLSGLVKKVNRRLKTIAVSDP  300

Qy  298  ASL  300
         ::|
Db  301  ETI  303
```

RESULT 13
US-10-282-122A-77375
; Sequence 77375, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77375
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77375

Query Match 43.3%; Score 657.5; DB 6; Length 312;

RESULT 14
US-10-369-493-17325
; Sequence 17325, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17325
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-369-493-17325

Query Match 43.1%; Score 654; DB 6; Length 313;
Best Local Similarity 45.6%; Pred. No. 8e-49;
Matches 141; Conservative 58; Mismatches 106; Indels 4; Gaps 4;

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Qy    1  MTKTAFLFAGQGAQYLGMGRDFYDQYPIVKETIDRASQVLGYDL-RYLIDTEEDKLNQTR   59
         | | :||||||||| :|||    :||     :  ||||| ||: |   |:|:|||||||:::
Db    1  MAKVAFLFPGQGSQSVGMGSELLSEEK-AKEIFDEADERLGYSLSSIMFEGPEKLRRTE   59

Qy   60  YTQPAILATSVAIYRLLQEKGYQPDMVAGLSGEYSALVASGALDFEDAVALVAKRGAYM  119
         :|||| | :| || : :|: | :|| | |||||||||||| :|:| ||| ||   |: |
Db   60  NTQPALLTMSTAVLSLVREYGIKPDYTAGHSLGEYSALVASGSLTFADAVYYAVHHRGLFM 119

Qy  120  EEAAPADSGKMVAVLNTPVEVIEEACQKASELG-VVTPANYNTPAQIVIAGEVVAVDRAV  178
         || |    |::||::|  : : :::|:| :: | ||   | :  ||||:||  :|  ||:
Db  120  EEAVPFGEGAMAAILGMERDELEQVTKRVTEAGAVVELANLNCPGQIVISGSAEGVEQAS  179

Qy  179  ELLQEAGAKRLIPLKVSGPFHTALLEPASQKLAETLAQVFSDFTCPLVGNTEAAVMQK-  237
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Search completed: June 11, 2003, 20:12:15
Job time : 81 secs
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RESULT 15
US-10-282-122A-68370
; Sequence 68370, Application US/10282122A
; GENERAL INFORMATION:
;    APPLICANT: Wang, Liangsu
;    APPLICANT: Zamudio, Carlos
;    APPLICANT: Malone, Cheryl
;    APPLICANT: Haselbeck, Robert
;    APPLICANT: Ohlsen, Kari
;    APPLICANT: Zyskind, Judith
;    APPLICANT: Wall, Daniel
;    APPLICANT: Trawick, John
;    APPLICANT: Carr, Grant
;    APPLICANT: Yamamoto, Robert
;    APPLICANT: Forsyth, R.
;    APPLICANT: Xu, H.
;    TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;    FILE REFERENCE: ELITRA.034A
;    CURRENT APPLICATION NUMBER: US/10/282,122A
;    CURRENT FILING DATE: 2003-02-20
;    PRIOR APPLICATION NUMBER: 60/191,078
;    PRIOR FILING DATE: 2000-03-21
;    PRIOR APPLICATION NUMBER: 60/206,848
;    PRIOR FILING DATE: 2000-05-23
;    PRIOR APPLICATION NUMBER: 60/207,727
;    PRIOR FILING DATE: 2000-05-26
;    PRIOR APPLICATION NUMBER: 60/230,335
;    PRIOR FILING DATE: 2000-09-06
;    PRIOR APPLICATION NUMBER: 60/230,347
;    PRIOR FILING DATE: 2000-09-09
;    PRIOR APPLICATION NUMBER: 60/242,578
;    PRIOR FILING DATE: 2000-10-23
;    PRIOR APPLICATION NUMBER: 60/253,625
;    PRIOR FILING DATE: 2000-11-27
;    PRIOR APPLICATION NUMBER: 60/257,931
;    PRIOR FILING DATE: 2000-12-22
;    PRIOR APPLICATION NUMBER: 60/267,636
;    PRIOR FILING DATE: 2001-02-09
;    PRIOR APPLICATION NUMBER: 60/269,308
;    PRIOR FILING DATE: 2001-02-16
;    Remaining Prior Application data removed - See File Wrapper or PALM.
;    NUMBER OF SEQ ID NOS: 78614
;    SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68370
;    LENGTH: 310
;    TYPE: PRT
;    ORGANISM: Proteus mirabilis
US-10-282-122A-68370

Query Match          42.8%;  Score 649.5;  DB 6;  Length 310;
Best Local Similarity  47.2%;  Pred. No. 1.9e-48;
Matches 145;  Conservative  51;  Mismatches 108;  Indels  3;  Gaps  3;

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Qy  119 MEEAAPADSGKMVAVLNTPVEVIEEACQXASELGVVTPANYNTPAQIVIAGEVVAVDRAV 178
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OM protein - nucleic search, using frame_plus_p2n model

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GenCore version 5.1.6

Run on: June 11, 2003, 20:17:43 ; Search time 2196 seconds
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Searched: 24791104 seqs, 12571243825 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1518	100.0	1518	17	921	US-09-308-397-1	Sequence 1, Appli
2	1518	100.0	1518	22	921	US-09-583-110-1251	Sequence 1251, Ap
3	1518	100.0	1518	29	921	US-09-752-069A-30	Sequence 30, Appl
4	1518	100.0	1518	61	924	US-60-174-088-30	Sequence 30, Appl
5	1518	100.0	1518	15	924	US-09-107-433-794	Sequence 794, App
6	1518	100.0	1518	41	19702	US-10-158-844-7	Sequence 7, Appli

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US-09-308-397-2 (1-306) x US-09-308-397-1 (1-921)

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Db    1  ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60

Qy   21  AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu   40
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Qy   41  GlyTyrAspLeuArgTyrLeuLeuAspThrGluLeuLeuAspLysLeuAsnGlnThrArgTyr   60
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Qy   61  ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLysGly   80
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Db  181  ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC  240

Qy   81  TyrGlnProAspMetValAlaGlyGlyLeuSerLeuGlyTyrSerAlaLeuValAlaSer  100
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Db  241  TATCAGCCTGATATGGTTGCTGGTGGTTTGTCTCTTGGATATTCTGCCTTGGTGGCCAGC  300

Qy  101  GlyAlaLeuAspPheGluAspAlaValAlaLeuAlaLeuAlaArgGlyValAlaTyrMetGlu  120
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Db  301  GGCGCGCCTTGGATTTGAAGATGCGGTTGCCTTGGTAGCGTGGAGCGTAAGGTATGGAA  360

Qy  121  GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal  140
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Db  361  GAAGCGGCTCCTGCTGACTCTCGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC  420

Qy  141  IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn  160
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Qy  161  ThrProAlaGlnIleValIleAlaGlyValGluValAlaAlaValAspArgAlaValGluLeu  180
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Qy  261  MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly  280
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Qy  281  PheValLysIleAspGlnThrAlaHisLeuAlaHisValGlnAspAlaSerLeu  300
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; Sequence 1251, Application US/09583110
; GENERAL INFORMATION:

(rotated left margin table)

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  17   952   62.7   2969  50  US-60-068-186-533         Sequence 533, App
  18   948   62.5    987  15  US-09-107-532-3319        Sequence 3319, Ap
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  20   937   61.7    942   1  PCT-US02-03987-6823       Sequence 6823, Ap
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  23   937   61.7    948  15  US-09-134-000-1582        Sequence 1582, Ap
  24   920   60.6   3656  14  US-09-070-927-577         Sequence 577, Appl
  25   920   60.6    920  17  US-09-070-927A-577        Sequence 577, Appl
  26   863   56.9    547   1  US-09-308-397-5           Sequence 5, Appli
  27   858   56.5   1196   1  PCT-US97-07950-8          Sequence 8, Appli
c 28   858   56.5   1199   2  US-08-832-030-78          Sequence 78, Appl
c 29   858   56.5   1209  16  US-09-297-451-81          Sequence 81, Appl
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  33   830   54.7   3627  50  US-60-068-217-803         Sequence 803, App
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  39   646   42.6    942  34  US-09-902-540-7357        Sequence 7357, Ap
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ALIGNMENTS

RESULT 1
US-09-308-397-1
; Sequence 1, Application US/09308397
; GENERAL INFORMATION:
; APPLICANT: Gentry, Daniel R.
; APPLICANT: Lonsdale, John T.
; APPLICANT: Payne, David J.
; APPLICANT: Pearson, Stewart C.
; APPLICANT: Van Aller, Glenn
; TITLE OF INVENTION: Novel FabD
; FILE REFERENCE: P50593
; CURRENT APPLICATION NUMBER: US/09/308,397
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: US 60/031,160
; EARLIER FILING DATE: 1996-11-18
; EARLIER APPLICATION NUMBER: PCT/US97/20992
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 921
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-308-397-1

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Alignment Scores:
Pred. No.:              921
Score:                  1518.00
Percent Similarity:     100.00%
Best Local Similarity:  100.00%
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Length:	921	
Matches:	306	
Conservative:	0	
Mismatches:	0	

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;    APPLICANT: Lynn Doucette-Stamm et al.
;    TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;    TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
;    FILE REFERENCE: PATH00-07A
;    CURRENT APPLICATION NUMBER: US/09/583,110
;    CURRENT FILING DATE: 2000-05-26
;    PRIOR APPLICATION NUMBER: US 09/107,433
;    PRIOR FILING DATE: 1998-06-30
;    PRIOR APPLICATION NUMBER: US 60/085,131
;    PRIOR FILING DATE: 1998-05-12
;    PRIOR APPLICATION NUMBER: US 60/051,553
;    PRIOR FILING DATE: 1997-07-02
;    NUMBER OF SEQ ID NOS: 5322
;    SEQ ID NO 1251
;      LENGTH: 921
;      TYPE: DNA
;      ORGANISM: Streptococcus pneumoniae
US-09-583-110-1251

Alignment Scores:
Pred. No.:                              1.58e-141
Score:                                  1518.00
Percent Similarity:                     100.00%
Best Local Similarity:                  100.00%
Query Match:                            100.00%
DB:                                     22

US-09-3,08-397-2  (1-306)  x  US-09-583-110-1251  (1-921)

Qy     1  MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg    20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCAGTATCTAGGGATGGGACGG    60

Qy    21  AspPheTyrAspGlnTyrProIleValLysGluThrIleAspAlaSerArgAlaSerGlnValLeu    40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GATTTCCATGATCAGTATCCGATTGTTAAAGAAACGATTGATGCGAGCCGAGTGCAGGTGCTC    120

Qy    41  GlyTyrAspLeuArgTyrLeuIleAspThrGluAspLysLeuAsnGlnThrArgTyr    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGGACAAACTCAATCAGACCCCCTAT    180

Qy    61  ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLysGly    80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ACGCAACCAGCCATTCTAGCGACTTCGGTCGCTATCTACCGTTATTGCAAGAAAAGGGC    240

Qy    81  TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer    100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TATCAGCCTGATATGGTCGCTGGTTTGTCTCTCGGGGAATACTCTGCCCTTGGTGGCAAGC    300

Qy   101  GlyAlaLeuAspPheGluAspAlaValAlaLeuAlaLysArgGlyAlaTyrMetGlu    120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301  GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA    360

Qy   121  GluAlaAlaProAlaAspSerGlyLysMetGlyLysAsnThrProValGluVal    140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361  GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCCAAATACGCCAGTAGAGGTC    420

Qy   141  IleGluGlyAlaCysGlnLysLysAlaSerGlnLeuGlyValValThrProAlaAsnTyrAsn    160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421  ATTGAAGGAGCCTGTCAAAAAGCTTCGCAACTTGGAGTGGTTACTCCAGCCAACTATAAC    480

Qy   161  ThrProAlaGlnIleValIleAlaGlyValAspValValAlaAlaLeuAspArgAlaValGluLeu    180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481  ACACCTGCACAAATCGTCATTGCTGGAGAAGCGGTTGCAGTGCGTTGAACTT    540

Qy   181  LeuGlnGluAlaGlyArgLeuLeuProLeuLysSerGlyProPheHisThr    200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541  TTGCAAGAGGCAGGTCGCCAAACGCTTCCTCTTAAGGTCGGTCCGTTCCACACC    600

Qy   201  AlaLeuLeuGluProAlaSerGlnLysLysAlaGluThrLeuGluAlaGlnValSerPheSer    220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  GCTCTCCTTGAGCCAGCTAGCCAGAAACTAGCTGAAACTCTGGAAGCTCAGGTAAGTTTTCA    660
```

```
Qy   221  AspPheThrCysProLeuValGlyAsnThrGluAlaAlaAlaValMetGlnLysGluAspIle    240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661  GATTTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT    720

Qy   241  AlaGlnLeuThrArgGlnValLysGluThrIleAspAlaSerArgPheTyrGluSerIleGlyVal    260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   721  GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTCATGAAAGTATTGGGGTC    780

Qy   261  MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyLeuProGlyLysValLeuSerGly    280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   781  ATGCAAGAAGCAGGCATAAGCAACTTTATCGAAGATTGGACCGGGGAAAGTCTTGTCAGGT    840

Qy   281  PheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu    300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   841  TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA    900

Qy   301  ValAlaLeuLeuGluLys    306
          ||||||||||||||||||
Db   901  GTAGCACTTTTAGAAAAA    918
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```
RESULT 3
US-09-752-069A-30
;    Sequence 30, Application US/09752069A
;    GENERAL INFORMATION:
;    APPLICANT: Dougherty, Thomas J.
;    APPLICANT: Pucci, Michael J.
;    APPLICANT: Dougherty, Brian A.
;    APPLICANT: Davison, Daniel B.
;    APPLICANT: Bruccoleri, Robert E.
;    APPLICANT: Thanassi, Jane A.
;    APPLICANT: Farmer II, Bennett T.
;    TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
;    TITLE OF INVENTION: FOR CELL VIABILITY AND THEIR USES
;    FILE REFERENCE: D0001NP
;    CURRENT APPLICATION NUMBER: US/09/752,069A
;    CURRENT FILING DATE: 2000-12-29
;    PRIOR APPLICATION NUMBER: 60/174,089
;    PRIOR FILING DATE: 1999-12-30
;    NUMBER OF SEQ ID NOS: 338
;    SOFTWARE: PatentIn Ver. 2.0
;    SEQ ID NO 30
;      LENGTH: 921
;      TYPE: DNA
;      ORGANISM: Streptococcus pneumoniae
US-09-752-069A-30

Alignment Scores:
Pred. No.:                              1.58e-141          Length:          921
Score:                                  1518.00            Matches:         306
Percent Similarity:                     100.00%            Conservative:      0
Best Local Similarity:                  100.00%            Mismatches:        0
Query Match:                            100.00%            Indels:            0
DB:                                     29                 Gaps:              0

US-09-308-397-2  (1-306)  x  US-09-752-069A-30  (1-921)

Qy     1  MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg    20
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Db     1  ATGACTAAAACAGCCTTTTTATTTGCTGTGCAAGGTGCCAGTATCTAGGGATGGGACGG    60

Qy    21  AspPheTyrAspGlnTyrProIleValLysGluThrIleAspAlaSerArgAlaSerGlnValLeu    40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  GATTTCCATGATCAGTATCCGATTGTTAAAGAAACGATTGATGCGAGCCGAGTGCAGGTGCTC    120

Qy    41  GlyTyrAspLeuArgTyrLeuIleAspThrGluAspLysLeuAsnGlnThrArgTyr    60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGGACAAACTCAATCAGACCCCGCTAT    180

Qy    61  ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLysGly    80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  ACGCAACCAGCCATTCTAGCGACTTCGGTCGCTATCTACCGTTATTGCAAGAAAAGGGC    240

Qy    81  TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer    100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  TATCAGCCTGATATGGTCGCTGGTTTGTCTCTCGGGGAATACTCTGCCCTTGGTGGCAAGC    300
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Query Match: 100.00%   Indels: 0
DB: 61   Gaps: 0

US-09-308-397-2 (1-306) x US-60-174-089-30 (1-921)

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Qy    1  MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg   20
Db    1  ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60

Qy   21  AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu   40
Db   61  GATTTCTATGATCAGTATCCGATTGTTAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC  120

Qy   41  GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr   60
Db  121  GGTTATGATTTGCGTTATCTCATCGATACGGAGGAAGACAAACTCAATCAGACCCGCTAT  180

Qy   61  ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGluLeuLysGly   80
Db  181  ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGGAAGAAAAGGGC  240

Qy   81  TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer  100
Db  241  TATCAGCCTGATATGGTCGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC  300

Qy  101  GlyAlaLeuAspPheGluAlaValAlaLeuLeuAlaLysArgGlyAlaTyrMetGlu     120
Db  301  GGCGCCCTTGGATTTGAAGCTGTAGCGCTGCTGGCTAAGCGTGGAGCCTATATGGAA     360

Qy  121  GluAlaAlaProAlaAspSerGlyLysMetValAlaValAlaLeuAsnThrProValGluVal  140
Db  361  GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTGCTCTTAATACGCCAGTAGAGGTC  420

Qy  141  IleGluGluAlaCysGlnLeuAlaSerGlyLeuValAlaValAlaValAlaLeuAsnTyrAsn  160
Db  421  ATTGAAGAAGCCTGTCAAAAAGCTTCAATACGCCAGTTCTCATACGGCCAACTATAAC  480

Qy  161  ThrProAlaGlnIleValIleGluAlaGlyLeuAlaGlyValValAlaAlaValAlaAspArgAlaArgValGluLeu  180
Db  481  ACACCTGCACAAATCGTCATTGCTGGAGGTTGCAGTGGTGGTTACTCCGACGTTGAACTT  540

Qy  181  LeuGlnGluLeuAlaGlyLeuAlaLysArgLeuIleSerGlyValSerProGlyPheHisThr  200
Db  541  TTGCAAGAAGCAGGTGCCAAACGCTTGATCTCTTAAGGTGTCCAGTGTCCCTTTCACACC  600

Qy  201  AlaAlaLeuLeuGluProAlaSerGlnLeuLysGluAlaGlnLeuThrLeuAlaGlnValSerPheSer  220
Db  601  GCTCTCCTTGAGCCAGCTAGCCAGAAACTAGCTGAAACTTAGCTGAAACTCAGGTAAGTTTTTCA  660

Qy  221  AspPheThrCysProLeuValGlyValAsnThrGlnAlaMetGlnLysGlnGlnLysGluAspIle  240
Db  661  GATTTTACTTGTCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAAAAGAGGACATT  720

Qy  241  AlaGlnLeuLeuThrArgGlnValValLysGluProValArgPheTyrGlnSerIleGlyVal  260
Db  721  GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC  780

Qy  261  MetGlnGluAlaGlyIleIleSerAsnPheIleLeuGluIleGlyProGlyLysValLeuSerGly  280
Db  781  ATGCAAGAAGCAGGCATAAGCAACCAACTTATCGAGATTGGACCGGGAAAGTCTTGTCAGGT  840

Qy  281  PheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGlyAspGlnAlaSerLeu  300
Db  841  TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA  900

Qy  301  ValAlaLeuLeuGluLys    306
Db  901  GTAGCACTTTTAGAAAAA    918
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RESULT 5
US-09-107-433-794
; Sequence 794, Application US/09107433
; GENERAL INFORMATION:

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Db  241  TATCAGCCTGATATGGTCGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC  300
Qy  101  GlyAlaLeuAspPheGluAlaValAlaLeuLeuAlaLysArgGlyAlaTyrMetGlu     120

Db  301  GGCGCCCTTGGATTTGAAGCTGTAGCGCTGCTGGCTAAGCGTGGAGCCTATATGGAA     360
Qy  121  GluAlaAlaProAlaAspSerGlyLysLeuLysMetValAlaValAlaLeuAsnThrProValGluVal  140

Db  361  GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTGCTCTTAATACGCCAGTAGAGGTC  420
Qy  141  IleGluGluAlaCysGlnLeuAlaSerGlyLeuValAlaValAlaValAlaLeuAsnTyrAsn  160

Db  421  ATTGAAGAAGCCTGTCAAAAAGCTTCAATACGCCAGTTCTCATACGGCCAACTATAAC  480
Qy  161  ThrProAlaGlnIleValIleGluAlaGlyLeuAlaGlyValValAlaAlaValAlaAspArgAlaArgValGluLeu  180

Db  481  ACACCTGCACAAATCGTCATTGCTGGAGGTTGCAGTGGTGGTTACTCCGACGTTGAACTT  540
Qy  181  LeuGlnGluLeuAlaGlyLeuAlaLysArgLeuIleSerGlyValSerProGlyPheHisThr  200

Db  541  TTGCAAGAAGCAGGTGCCAAACGCTTGATCTCTGGTGTCAGTCCTGGTTTCCACACC  600
Qy  201  AlaAlaLeuLeuGluProAlaSerGlnLeuLysGluAlaGlnLeuThrLeuAlaGlnValSerPheSer  220

Db  601  GCTCTCCTTGAGCCAGCTAGCCAGAAACTAGCTGAAACTCAGGTAAGTTTTTCA  660
Qy  221  AspPheThrCysProLeuValGlyValAsnThrGlnAlaMetGlnLysGlnGlnLysGluAspIle  240

Db  661  GATTTTACTTGTCCCCTAGTCGGCAATACAGAGAGCTGCTGTGATGCAAAAGAGGACATT  720
Qy  241  AlaGlnLeuLeuThrArgGlnValValLysGluProValArgPheTyrGlnSerIleGlyVal  260

Db  721  GCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC  780
Qy  261  MetGlnGluAlaGlyIleIleSerAsnPheIleLeuGluIleGlyProGlyLysValLeuSerGly  280

Db  781  ATGCAAGAAGCAGGCATAAGCAACCAACTTATCGAGATTGGACCGGGAAAGTCTTGTCAGGT  840
Qy  281  PheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGlyAspGlnAlaSerLeu  300

Db  841  TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA  900
Qy  301  ValAlaLeuLeuGluLys    306

Db  901  GTAGCACTTTTAGAAAAA    918
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Alignment Scores:			
Pred. No.:		Length:	921
Score:	1.58e-141 1518.00	Matches:	306
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
        SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
        THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
        ADDRESSEE: GENOME THERAPEUTICS CORPORATION
        STREET: 100 Beaver Street
        CITY: Waltham
        STATE: Massachusetts
        COUNTRY: USA
        ZIP: 02354
COMPUTER READABLE FORM:
        MEDIUM TYPE: CD/ROM ISO9660
        COMPUTER: <Unknown>
        OPERATING SYSTEM: <Unknown>
        SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/107,433
        FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 60/085131
        FILING DATE: May 12, 1998
        APPLICATION NUMBER: 60/051553
        FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
        NAME: Ariniello, Pamela Deneke
        REGISTRATION NUMBER: 40,489
        REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
        TELEPHONE: (781)893-5007
        TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 794:
SEQUENCE CHARACTERISTICS:
        LENGTH: 924 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
        ORGANISM: Streptococcus pneumoniae
FEATURE:
        NAME/KEY: misc feature
        LOCATION: (B) LOCATION 1...924
SEQUENCE DESCRIPTION: SEQ ID NO: 794:
US-09-107-433-794

Alignment Scores:
Pred. No.:
Score: 1.58e-141   Length: 924
                       1518.00   Matches: 306
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 15   Gaps: 0

US-09-308-397-2 (1-306) x US-09-107-433-794 (1-924)

Qy   1 MetThrIleThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4 ATGACTAAAACAGCCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 63

Qy   21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 GATTTCTATGATCAGTATCCGATTGTTAAAGAAACGATTGATCGAGCGAGTCAGGTGCTC 123

Qy   41 GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 124 GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGGACAAACTCAATCAGACCCGCTAT 183

Qy   61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleThrSerValAlaIleTyrArgLeuGlnLeuGlnLysGly 80
          |||||||||||||||||||||||||||

Db 184 ACGCAACCAGCCATTCTACGACTTCGGTGCTATCTACCGTTTATTGCAAGAAAAAGGGC 243

Qy   81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaLeuSer 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 244 TATCAGCCTGATATGGTCGCTGGTTTGTCTCTTGGAGAATACTCTGCCTTGGTGTGCAAGC 303

Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuAlaLeuLysArgGlyAlaTyrMetGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 304 GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 363

Qy 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 364 GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 423

Qy 141 IleGluGlnAlaCysGlnLysSerGluLeuGlyValValThrProAlaAsnTyrAsn 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 424 ATTGAGCAAGCCTGTCAAAAAGCTTCAAAAGCTTCCAGCCAACTATAAC 483

Qy 161 ThrProAlaGlnIleValIleAlaGlyGluValAlaValAlaValAspArgArgAlaValGluLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 484 ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGCTGACCGTCGAGCTGAACTT 543

Qy 181 LeuGlnGluAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyValProPheHisThr 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 544 TTGCAAGAAGCAGGTGCCAAACGCTTGATTCCTCTTAAGGTGTCAGGTGTCCCTTTCACACC 603

Qy 201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGlyThrLeuAlaGlnIleValSerPheSer 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 604 GCTCTCCTTGAGCCAGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGTAAGTTTTTCA 663

Qy 221 AspPheThrProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluIle 240
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Db 664 GATTTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGACATT 723

Qy 241 AlaGlnLeuLeuThrArgGlnValLysGluTyrGluSerIleGlyVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db 724 GCTCAGCTCCTGACGCGTCAGGTCAAGGAACCCGTTCGTTCTATGAAAGTATTGGGGTC 783

Qy 261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 784 ATGCAAGAAGCAGGCATAAGCAACTTATCGAGATTGACCGGGAAAGTCTTCAGGT 843

Qy 281 PheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 844 TTTGTTAAAAAAATTGATCAAACTGCTCACTTAGCTCACGTGGAAGATCAAGCGAGTTTA 903

Qy 301 ValAlaLeuLeuGluGluLys 306
          |||||||||||||||||||||
Db 904 GTAGCACTTTTAGAAAAA 921

RESULT 6
US-10-158-844-7/c
; Sequence 7, Application US/10158844
; GENERAL INFORMATION:
        APPLICANT: Kunsch et al.
        TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
        NUMBER OF SEQUENCES: 391
        CORRESPONDENCE ADDRESS:
                ADDRESSEE: Human Genome Sciences, Inc.
                STREET: 9410 Key West Avenue
                CITY: Rockville
                STATE: Maryland
                COUNTRY: USA
                ZIP: 20850
        COMPUTER READABLE FORM:
                MEDIUM TYPE: CD-R
                COMPUTER: Dell Latitude Pentium 3
                OPERATING SYSTEM: Windows 98
                SOFTWARE: ASCII Text
        CURRENT APPLICATION DATA:
                APPLICATION NUMBER: US/10/158,844
                FILING DATE: 03-Jun-2002
                CLASSIFICATION: <Unknown>

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     PRIOR APPLICATION DATA:
        APPLICATION NUMBER: US 08/961,527
          FILING DATE: 1997-10-30
        APPLICATION NUMBER: US 60/029,960
          FILING DATE: 1996-10-31
     ATTORNEY/AGENT INFORMATION:
        NAME: Hyman, Mark J.
        REGISTRATION NUMBER: 46,789
        REFERENCE/DOCKET NUMBER: PB340P1D1
  INFORMATION FOR SEQ ID NO: 7:
     SEQUENCE CHARACTERISTICS:
        LENGTH: 19702 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
     SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-158-844-7

Alignment Scores:
Pred. No.:                          6.46e-140        Length:        19702
Score:                              1518.00          Matches:       306
Percent Similarity:                 100.00%          Conservative:  0
Best Local Similarity:              100.00%          Mismatches:    0
Query Match:                        100.00%          Indels:        0
DB:                                 41               Gaps:          0

US-09-308-397-2 (1-306) x US-10-158-844-7 (1-19702)

Qy      1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg  20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17149 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG  17090

Qy     21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaserGlnValLeu  40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17089 GATTTCTATGATCAGTATCCGATTGTTAAAGAAACGATTGATGGAGCGAGCCAGTGCTC  17030

Qy     41 GlyTyrAspLeuArgThrValGlyTyrLeuIleAspGluThrGluGlnLeuAsnGlnThrArgTyr  60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17029 GGTTATGATTTGCGTTATCTATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT  16970

Qy     61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLysGly  80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16969 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC  16910

Qy     81 TyrGlnProAspMetValAlaGlyValLeuSerLeuGlyGluThrTyrSerAlaLeuValAlaSer  100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16909 TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGATACCTGCCTTGGTGGCAAGT  16850

Qy    101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrAlaTyrMetGlu  120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16849 GGCGCCTTGGATTTTGAAGATGCGGTGCCTTGGCTAAGCGTGGAGCCTATATGGAA  16790

Qy    121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal  140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16789 GAAGCGGCTCCTGCTGACTCCGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGTC  16730

Qy    141 IleGluGluIleGluLysAlaCysGlnLysAlaSerAlaSerGlyLeuGlyValValThrProAlaAsnTyrAsn  160
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16729 ATTGAAGAAGCCTGTCAAAAAGCTTCTGCAAGCTCTGACTTGGAGTGGTTACTCCAGCCAACTATAAC  16670

Qy    161 ThrProAlaGlnIleIleValIleLeuAlaGlyGluValGlyValValAlaAspArgAlaValAlaGluLeu  180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16669 ACACCTGCACAAATCGTCATTGCTGGAGAGTGGTTGCAGTTGATCGAGCGGTTGAACTT  16610

Qy    181 LeuGlnGluAlaGlyAlaValLysArgGluIleProLeuLysSerGlyProPheHisThr  200
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16609 TTGCAAGAAGCAGGTGCCAAACGCTTGAATCCTTTAAGGTGTGCAAGGTGCCCCTTTTCACACC  16550

Qy    201 AlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaValSerPheSer  220
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16549 GCTCTTCCTGAACCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGTAAGTTTTCA  16490

Qy    221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle  240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17155 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG  17096
```

Right column:

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Db  16489 GATTTTACTTGTCCCCTAGTCGGCAATACAGAAGGTGCTGTGATGCAAAAGAGAGACATT  16430

Qy    241 AlaGlnLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal  260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16429 GCTCAGCTCTTGACGCGTCAGGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC  16370

Qy    261 MetGlnGlyAlaGlyIleSerAsnPheIleGluGluIleGlyProGlyLysValLeuSerGly  280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16369 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAAGATTGGACCGGGGAAAGTCTTGTCAGGT  16310

Qy    281 PheValLysIleAspSerGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  16309 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA  16250

Qy    301 ValAlaLeuLeuGluLys  306
            ||||||||||||||||||
Db  16249 GTAGCACTTTTAGAAAAA  16232
```

```
RESULT 7
US-60-029-960-61/c
  Sequence 61, Application US/60029960
  GENERAL INFORMATION:
     APPLICANT: Charles Kunsch
     TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
     NUMBER OF SEQUENCES: 1649
     CORRESPONDENCE ADDRESS:
        ADDRESSEE: Human Genome Sciences, Inc.
        STREET: 9410 Key West Avenue
        CITY: Rockville
        STATE: Maryland
        COUNTRY: USA
        ZIP: 20850
     COMPUTER READABLE FORM:
        MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
        COMPUTER: HP Vectra 486/33
        OPERATING SYSTEM: MSDOS version 6.2
        SOFTWARE: ASCII Text
     CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/60/029,960
        FILING DATE:
     CLASSIFICATION:
     PRIOR APPLICATION DATA:
        APPLICATION NUMBER:
        FILING DATE:
     ATTORNEY/AGENT INFORMATION:
        NAME: Brookes, A. Anders
        REGISTRATION NUMBER: 36,373
        REFERENCE/DOCKET NUMBER: PB340PP
     TELECOMMUNICATION INFORMATION:
        TELEPHONE: (301) 309-8504
        TELEFAX: (301) 309-8512
  INFORMATION FOR SEQ ID NO: 61:
     SEQUENCE CHARACTERISTICS:
        LENGTH: 19706 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
US-60-029-960-61

Alignment Scores:
Pred. No.:                          6.46e-140        Length:        19706
Score:                              1518.00          Matches:       306
Percent Similarity:                 100.00%          Conservative:  0
Best Local Similarity:              100.00%          Mismatches:    0
Query Match:                        100.00%          Indels:        0
DB:                                 46               Gaps:          0

US-09-308-397-2 (1-306) x US-60-029-960-61 (1-19706)

Qy      1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg  20
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  17155 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG  17096
```

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;   TITLE OF INVENTION:  FOR CELL VIABILITY AND THEIR USES
;   FILE REFERENCE: D0001NP
;   CURRENT APPLICATION NUMBER: US/09/752,069A
;   CURRENT FILING DATE:   2000-12-29
;   PRIOR APPLICATION NUMBER: 60/174,089
;   PRIOR FILING DATE: 1999-12-30
;   NUMBER OF SEQ ID NOS: 338
;   SOFTWARE: PatentIn Ver. 2.0
;
;   SEQ ID NO 256
;   LENGTH: 945
;   TYPE: DNA
;   ORGANISM: Streptococcus pneumoniae
US-09-752-069A-256

Alignment Scores:
Pred. No.:                 3.24e-141       Length:              945
Score:                     1515.00         Matches:             305
Percent Similarity:        100.00%         Conservative:          1
Best Local Similarity:     99.67%          Mismatches:            0
Query Match:               99.80%          Indels:                0
DB:                        29              Gaps:                  0

US-09-308-397-2 (1-306)  x  US-09-752-069A-256  (1-945)
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Qy      1  MetThrLysThrAlaPheLeuPheAlaGlyValGlnGlyAlaGlnTyrLeuGlyMetGlyArg    20
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  ATGACTAAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCCTAGGGATGGGACGG    60

Qy     21  AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu      40
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61  GATTTCATGATCAGTATCCGATTGTAAAGAACAGATTGAGCGCAGTCAGGTGCTA        120

Qy     41  GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr      60
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121  GGTTATGATTTGCGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT     180

Qy     61  ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnLysLysGly      80
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    181  ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC     240

Qy     81  TyrGlnProAspMetValAlaGlyLeuSerLeuGlyTyrSerAlaLeuValSer          100
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241  TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGATACTCTGCTTTGGTGGCAAGC       300

Qy    101  GlyAlaAlaLeuAspPheGluAspAlaAlaLeuAlaLeuAlaLeuAlaLysArgGlyAlaTyrMetGlu   120
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    301  GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGCAGCTGCGTGGAGCCTATATGGAA     360

Qy    121  GluAlaAlaProAlaAspSerGlyLysMetValAlaLeuAsnThrProValGluVal        140
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    361  GAAGCGGCTCCTGCTGACTCGGCAAGATGGTAGCAGTTCCAATACGCCAGTAGAGGTC     420

Qy    141  IleGluGluAlaCysGlnLysAlaSerGluLeuAlaGluThrLeuAlaGlnValSerPheSer  160
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    421  ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGCTACTCTGGCTCAGGTTTCTTCA   480

Qy    161  ThrProAlaGlnIleValIleAlaGlyLysValAspArgLeuIleProLeuAlaArgAlaValGluLeu  180
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    481  ACACCTGCACAAATCGTCATTGCTGGGAAGGTGGTTGCAGTTGATGCGAGCCGTTGAACTT   540

Qy    181  LeuGlnGluAlaGlyValAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr  200
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    541  TTGCAAGAGGCAGGTGCCAAACGCTTAATCCCTCTTAAGGTGTCAGGTCCCTTTCACACC   600

Qy    201  AlaLeuLeuGluProAlaSerGlyLysValProLeuAlaGluThrLeuAlaGlnValSerPheSer  220
           : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    601  TCTCTCCTTGAACCTGCTAGCCAGAAACTAGCTGAACTCTGGCTCAGGTAAGTTTTTCA   660

Qy    221  AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle  240
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    661  GATTTTACTTGTCCCCTAGTGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT   720

Qy    241  AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrArgPheTyrGluSerIleGlyVal   260
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Qy     21  AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu      40
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  17095  GATTTCATGATCAGTATCCGATTGTAAAGAACAGATTGAGCGCAGTCAGGTGCTC      17036

Qy     41  GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr      60
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  17035  GGTTATGATTTGCGTTATCTCATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT     16976

Qy     61  ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnLysLysGly      80
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16975  ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC     16916

Qy     81  TyrGlnProAspMetValAlaGlyLeuSerLeuGlyTyrSerAlaLeuValAlaSer          100
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16915  TATCAGCCTGATATGGTTGCTGGTTTGTCTCTTGGAGAATACTCTGCTTGGTGGGCAAGT     16856

Qy    101  GlyAlaAlaLeuAspPheGluAspAlaAlaLeuAlaLeuAlaLeuAlaLysArgGlyAlaTyrMetGlu   120
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16855  GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGCAGCTGCGTGGAGCCTATATGGAA     16796

Qy    121  GluAlaAlaProAlaAspSerGlyLysMetValAlaLeuAsnThrProValGluVal        140
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16795  GAAGCGGCTCCTGCTGACTCGGCAAGATGGTAGCAGTTCCAATACGCCAGTAGAGGTC     16736

Qy    141  IleGluGluAlaCysGlnLysAlaSerGluLeuAlaGluThrLeuAlaGlnValSerPheSer  160
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16735  ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGCTACTCTGGCTCAGGTAAGTTTTTCA   16676

Qy    161  ThrProAlaGlnIleValIleAlaGlyLysValAspArgLeuIleProLeuAlaArgAlaValGluLeu  180
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16675  ACACCTGCACAAATCGTCATTGCTGGGAAGGTGGTTGCAGTTGATCGAGCCGTTGAACTT     16616

Qy    181  LeuGlnGluAlaGlyValAlaLysArgLeuIleProLeuLysValSerGlyProPheHisThr  200
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16615  TTGCAAGAGGCAGGTGCCAAACGCTTAATCCCTCTTAAGGTGTCAGGTCCCTTTCACACC   16556

Qy    201  AlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSer  220
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16555  GCTCTCCTTGAACCTGCTAGCCAGAAACTAGCTGAACCTCAGTAAGTTTTTCA        16496

Qy    221  AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle  240
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16495  GATTTTACTTGTCCCCTAGTCGGCAATACAGAGCTGCTGTGATGCAAAAAGAGGACATT   16436

Qy    241  AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrArgPheTyrGluSerIleGlyVal   260
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16435  GCTCAGCTCCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTCATGAAAGTATTGGGGTC     16376

Qy    261  MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly      280
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16375  ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCCGGGAAAGTCTTGTCAGGT     16316

Qy    281  PheValLysLysGluAspPheAsnPheIleAlaHisLeuAlaHisGlnAlaSerLeu      300
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  16315  TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGAAGATCAAGCGAGTTTA    16256

Qy    301  ValAlaLeuGluLys  306
           | | | | | | | | | | |
Db  16255  GTAGCACTTTTAGAAAAA  16238
```

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RESULT 8
US-09-752-069A-256
;    Sequence 256, Application US/09752069A
;    GENERAL INFORMATION:
;    APPLICANT:  Dougherty, Thomas J.
;    APPLICANT:  Pucci, Michael J.
;    APPLICANT:  Dougherty, Brian A.
;    APPLICANT:  Davison, Daniel B.
;    APPLICANT:  Bruccoleri, Robert E.
;    APPLICANT:  Thanassi, Jane A.
;    APPLICANT:  Farmer II, Bennett T.
;    TITLE OF INVENTION: NOVEL BACTERIAL GENES AND PROTEINS THAT ARE ESSENTIAL
```

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Db      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    721 GCTCAGCTCCTTGACGCGCTCAGGTCAGGAACCCGTTCGTTCGTTTCATGAAAGTATTGGGGTC 780

Qy  261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
Db  781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTCTTGTCAGGT 840

Qy  281 PheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu 300
Db  841 TTTGTTAAAAAATTGATCAAAACGCTCACTTAGCTCAGTTCATGTGGAAGATCAAGCGAGTTTA 900

Qy  301 ValAlaLeuGluLys 306
Db  901 GTAGCACTTTTAGAAAAA 918
```

RESULT 9
PCT-US97-22578-43
; Sequence 43, Application PC/TUS9722578
  GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Burgett, Stanley G.
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Jaskunas Jr., Stanley R.
; APPLICANT: Mills, Bradley J
; APPLICANT: Norris, Franklin H.
; APPLICANT: Peery, Robert B.
; APPLICANT: Rosteck Jr., Paul R.
; APPLICANT: Skatrud, Paul L.
; APPLICANT: Smith, Michele C.
; APPLICANT: Rockey, Pamela K.
; APPLICANT: Young-Bellido, Michele
; TITLE OF INVENTION: Streptococcus Pneumoniae DNA Sequences
; NUMBER OF SEQUENCES: 228
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Eli Lilly and Company
;   STREET: Lilly Corporate Center
;   CITY: Indianapolis
;   STATE: Indiana
;   COUNTRY: U.S.
;   ZIP: 46285
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: PCT/US97/22578
;   FILING DATE:
;   CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Webster, Thomas D.
;   REGISTRATION NUMBER: 39,872
;   REFERENCE/DOCKET NUMBER: X-11162
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 317-276-3334
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 3580 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US97-22578-43

Alignment Scores:
Pred. No.:   1.63e-140
Score: 1515.00
Percent Similarity: 100.00%
Best Local Similarity: 99.67%
Query Match: 99.80%

Length: 3580
Matches: 305
Conservative: 1
Mismatches: 0
Indels: 0
Gaps: 0

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US-09-308-397-2 (1-306) x PCT-US97-22578-43 (1-3580)

Qy    1 MetThrLysThrAlaPheLeuPheAlaGlyValGlyAsnGlyAlaGlnTyrLeuGlyMetGlyArg 20
Db  718 ATGACTAAAACAGCCTTTTTATTTGCTGGTGTCGGTAATGGTGCCCAGTATCTAGGGATGGGACGG 777

Qy   21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnAlaValLeu 40
Db  778 GATTTCTATGATCAGTATCCGATTGTTAAAGAAACAATTGATCGAGCGAGTCAGGCTGCTA 837

Qy   41 GlyTyrAspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyr 60
Db  838 GGTTATGATTTGCGTTATCTAATCGATACGGAAGAAGACAAACTCAATCAGACCCGCTAT 897

Qy   61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLysGly 80
Db  898 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC 957

Qy   81 TyrGlnProAspMetValAlaGlyLeuGluTyrSerAlaLeuValAlaSer 100
Db  958 TATCAGCCTGATATGGTTGCTGGTTTGGTCTCTGCTCTGGAAATACTTCCTGCCTTGGTGCAAGC 1017

Qy  101 GlyAlaLeuAspPheGluUsProAlaValAlaLeuAlaLeuAlaLysArgGlyAlaTyrMetGlu 120
Db 1018 GGGGCCCTTGGATTTGAAGATGGGGTTGCCTGGTAGCTAAGCGTGGAGCCTATATGGAA 1077

Qy  121 GluAlaAlaProAlaAspSerGlyLysMetValAlaAlaValLeuAsnThrProValGluVal 140
Db 1078 GAAGCGGCTCCTGCTACCTCGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 1137

Qy  141 IleGluGluAlaCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn 160
Db 1138 ATTGAAGAAGCCTGCAAAAAGCTTCGAACTTGGAGTGGTTACTCACTGCCAACTATAAC 1197

Qy  161 ThrProAlaGlnIleValIleAlaGlyGluValIleValAlaAlaValAspArgAlaValGluLeu 180
Db 1198 ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGCAGTCGAGCGGTTGAACTT 1257

Qy  181 LeuGlnLeuAlaGlyLysAlaLysArgLeuIleLeuProLeuLysValSerGlyValProHisThr 200
Db 1258 TTGCAAGAAGCAGGTGCCAAACGCTGATTCCTTAAGGTGTCAGGTCCCTTTCCACACC 1317

Qy  201 AlaLeuGluGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSer 220
Db 1318 TCTCTCCCTTGAACCTGCTAGCCAGAAACTAGCTGAAACTCTGGCTCAGGTAAGTTTTCA 1377

Qy  221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaAlaValMetGlnLysGluAspIle 240
Db 1378 GATTTTACTTGTCCCGAGTGGCAATACAGAAGCTGCTGTGATGCAAAAGAGGACATT 1437

Qy  241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
Db 1438 GCTCAGCTTCTTGACGCGTAGCCAGTCAAGGAACCCGTTCGTTTCTCATGAAAGTATTGGGGTC 1497

Qy  261 MetGlnGluAlaGlyIleSerAsnPheIleGlyIleGlyProGlyLysValLeuSerGly 280
Db 1498 ATGCAAGAAGCAGGCATAAGCAACTTTATCGGGATTGGACCCGGGAAAGTCTTGTCAGGT 1557

Qy  281 PheValLysIleAspGlnThrAlaHisLeuAlaHisLeuValAspGlnAlaSerLeu 300
Db 1558 TTTGTTAAAAAATTGATCAAACTGCTCACTTAGCTCATGTGGAAGATCAAGCGAGTTTA 1617

Qy  301 ValAlaLeuGluLys 306
Db 1618 GTAGCACTTTTAGAAAA 1615
```

RESULT 10
PCT-US02-03987-9482
; Sequence 9482, Application PC/TUS0203987
  GENERAL INFORMATION:
; APPLICANT: Elitra Pharmaceuticals, Inc.
; TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits

```
;  TITLE OF INVENTION: Proliferation
;  FILE REFERENCE: ELITRA.028VPC
;  CURRENT APPLICATION NUMBER: PCT/US02/03987
;  CURRENT FILING DATE: 2002-02-02
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  NUMBER OF SEQ ID NOS: 15811
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 9482
;  LENGTH: 921
;  TYPE: DNA
;  ORGANISM: Streptococcus pneumoniae
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(921)
PCT-US02-03987-9482
```

Alignment Scores:
```
Pred. No.:            3.96e-141
Score:               1514.00
Percent Similarity:   100.00%
Best Local Similarity: 99.67%
Query Match:          99.74%
DB:
```

US-09-308-397-2 (1-306) x PCT-US02-03987-9482 (1-921)

```
Qy      1  MetThrLysThrAlaPheLeuPheAlaGlyAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyTyrArg   20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ATGACTAAAACAGCCTTTTTATTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG               60

Qy     21  AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgArgAlaSerGlnValLeu          40
           |||||||||||||||||||||||||||||||||||||||||
Db     61  GATTTCTATGATCAGTATCCGATTGTCAAGAAAACGATTGATCGAGCGAGTCAGGTGCTA              120

Qy     41  GlyTyrTyrAspLeuArgTyrLeuIleAspThrGluGluAsnGlnThrArgTyr                   60
           |||||||||||||||||||||||||
Db    121  GGTTATTATGATTTGCGTTATCTCATCGATACGAAGAGGACAAACTCAATCAGACCCGCTAT           180

Qy     61  ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnLeuLysGly             80
           ||||||||||||||||||||||||||
Db    181  ACGCAACCAGCCATTCGAGGACTTCGGTTGCTATCATCCACCGTTATTGCAAGAAAAGGGC           240

Qy     81  TyrGlnProAspMetValAlaGlyLeuLeuSerLeuGlyTyrSerAlaLeuValAlaSer            100
           ||||||||||||||||||||||
Db    241  TATCAGCCTGATATGGTTGCTGGTTTGCTCGTTTGTCTCTTGGAGAATACCTCTGCCTTG          300

Qy    101  GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLeuLysArgGlyAlaTyrMetGlu         120
           |||||||||||||||||||||||||||||||||||||
Db    301  GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA          360

Qy    121  GluAlaAlaProAlaAspSerGlyLysMetValAlaMetThrProValGluVal               140
           ||||||||||||||||||||||||
Db    361  GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAAATACGCCAACTATAAC         420

Qy    141  IleGluGluAlaCysGlnLysAlaSerGluGluLeuGlyLeuGlyValValAlaAlaValAlaAspArgAlaValGluLeu  180
           ||||||||||||||||||||||||||||||||||||||||
Db    421  ATTGAAGAAGCCTGTCAAAAAGCTTCTGAACTTGGAGTGGTTACTCCAGCCAACTATAAC         480

Qy    161  ThrProAlaGlnIleValIleValIleAlaGlyValValAlaAlaValAlaValAspArgAlaValGluLeu          180
           ||||||||||||||||||||||||||||
Db    481  ACACCTGCACAAATCGTCATTGCTGGAGTGGTTGCAGTTGATCGAGCCGTTGAACTT             540

Qy    181  LeuGlnGluAlaGlyAlaGlyLysArgLeuIleProLeuLysValSerGlyValSerGlyProPheHisThr           200
           ||||||||||||||||||||||||
Db    541  TTGCAAGAAGCAGGTGCCAAACCCTTCAATCCTTAAGGTGTCAGGTGTCCCTTTCACACC          600

Qy    201  AlaLeuLeuGluProAlaSerGlnLysLeuLeuAlaGluThrLeuAlaGlnValSerPheSer          220
           ||||||||||||||||||||||||
Db    601  GCTCTCCTTGAACCTGCTAGCCAGAAACTAGCTGAAACTCTAGCTCAGGTAAGTTTTTCA         660

Qy    221  AspPheThrCysProLeuValGlyAsnThrGluAlaValMetGlnLysGluAspIle               240
           ||||||||||||||
Db  ... ATGACTAAAACAGCAGCCTTTTTATTTGCTGTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG    60
```

```
Db    661  GATTTACTTGTCCCCTAGTCGGCAATACAGAAGTGCTGTGATGCAAAAAGAGAGACATT        720

Qy    241  AlaGlnLeuLeuThrArgGlnValLysGluTyrGluSerIleGlyVal                     260
           ||||||||||||||||||||||||||||
Db    721  GCTCAGCTCTTGACGCGGTCAGGTCAAGGTCAAGGACCCGTTCGTTCTCATGAAAGTATTGGGGTC    780

Qy    261  MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly        280
           ||||||||||||||||||||||||||||
Db    781  ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTTTGTCAGGT          840

Qy    281  PheValLysSerIleAspGlnThrAlaHisLeuAlaHisLeuValGluValGlnAlaSerLeu      300
           ||||||||||||||||||||||||:::
Db    841  TTTGTTAAAAAAATTGATCGAACTGCTCACTTAGCTCATCTGGAAGATCAAGCGAGTTTA        900

Qy    301  ValAlaLeuLeuGluLys                                                   306
           ||||||||||||
Db    901  GTAGCACTTTTAGAAAAA                                                   918
```

RESULT 11
US-09-815-242-9482
```
;  Sequence 9482, Application US/0915242
;  GENERAL INFORMATION:
;  APPLICANT: Haselbeck, Robert
;  APPLICANT: Ohlsen, Kari L.
;  APPLICANT: Zyskind, Judith W.
;  APPLICANT: Wall, Daniel
;  APPLICANT: Trawick, John D.
;  APPLICANT: Carr, Grant J.
;  APPLICANT: Yamamoto, Robert T.
;  APPLICANT: Xu, H. Howard
;  TITLE OF INVENTION: Identification of Essential Genes in
;  TITLE OF INVENTION: Prokaryotes
;  FILE REFERENCE: ELITRA.011A
;  CURRENT APPLICATION NUMBER: US/09/815,242
;  CURRENT FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  NUMBER OF SEQ ID NOS: 14110
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 9482
;  LENGTH: 921
;  TYPE: DNA
;  ORGANISM: Streptococcus pneumoniae
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(921)
US-09-815-242-9482
```

Alignment Scores:
```
Pred. No.:            3.96e-141          Length:        921
Score:               1514.00            Matches:       305
Percent Similarity:   100.00%           Conservative:    1
Best Local Similarity: 99.67%           Mismatches:      0
Query Match:          99.74%            Indels:          0
DB:                       31            Gaps:            0
```

US-09-815-242-9482 (1-306) x US-09-815-242-9482 (1-921)

```
Qy      1  MetThrLysThrAlaPheLeuPheAlaGlyAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyTyrArg   20
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ATGACTAAAACAGCAGCCTTTTTATTTGCTGTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG      60
```

APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Roemer, Terry
APPLICANT: Jiang, Bo
APPLICANT: Bussey, Howard
APPLICANT: Boone, Charles
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9482
  LENGTH: 921
  TYPE: DNA
  ORGANISM: Streptococcus pneumoniae
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)...(921)
.US-10-072-851-9482

Alignment Scores:
Pred. No.:   921
Score: 3.96e-141   1514.00
Percent Similarity: 100.00%   Matches: 305
Best Local Similarity: 99.67%   Conservative: 1
Query Match: 99.74%   Mismatches: 0
DB: 39   Indels: 0
                                     Gaps: 0

US-09-308-397-2 (1-306) x US-10-072-851-9482 (1-921)

Qy   1 MetThrLysThrAlaPheLeuPheAlaGlyTyrGlnGlyAlaGlnTyrLeuGlyMetGlyArg   20
Db   1 ATGACTAAAACAGCCTTTTTATTTGCTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG   60

Qy   21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu   40
Db   61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTA   120

Qy   41 GlyTyrAspLeuArgTyrLeuIleAspThrGluLeuLeuAspLysLeuAsnGlnThrArgTyr   60
Db 121 GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGGACAAACTCAATCAGACCCGCTAT   180

Qy   61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLysGly   80
Db 181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC   240

Qy   81 TyrGlnProAspMetValAlaGlyValGlyTyrSerLeuGlyTyrSerAlaLeuValAlaSer   100
Db 241 TATCAGCCTGATATGGTTGCTGGTGTTGTCTTTGGAGAATACTCGCCTTGGTTGGCAAGC   300

Qy 101 GlyAlaLeuAspPheGluAspAlaAspSerGlyIleLysLysLysAlaLeuAlaArgGlyValAlaTyrMetGlu   120
Db 301 GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCCTAAGCGTGGAGCCTATATGAA   360

Qy 121 GluAlaAlaProAlaAspSerGlyLysLysMetValAlaAlaValLeuAsnThrProValGluVal   140
Db 361 GAAGCGGCTCCTGCTGACTCCGGCAAGATGGTGGCAGCAGTTCTCAATACGCCAGTAGAGGTC   420

Qy 141 IleGluGluAlaCysGlnLysLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn   160
Db 421 ATTGAAGAAGCCTGTCAAAAAGCTTCGAACTTGGAGTGGTTACTCCAGCCAACTATAAC   480

Qy 161 ThrProAlaGlnIleValIleAlaGlyGluValAlaValAlaAspArgAlaValGluLeu   180
Db 481 ACACCTGCACAAATCGTCATTGCTGGAGAGGTTGCAGTCGCGGTTGAACTT   540

Qy 181 LeuGlnGluLeuAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyValProHisThr   200
Db 541 TTGCAAGAGCAGGTGCCAAAGCGTTGATTCCTCTTAAGGTGTCAGGTCCCTTTCACC   600

RESULT 12
US-10-072-851-9482
; Sequence 9482, Application US/10072851
; GENERAL INFORMATION:
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel

Qy   21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu   40
Db   61 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGGTGCTA   120

Qy   41 GlyTyrAspLeuArgTyrLeuIleAspThrGluLeuLeuAspLysLeuAsnGlnThrArgTyr   60
Db 121 GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGGACAAACTCAATCAGACCCGCTAT   180

Qy   61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLysGly   80
Db 181 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC   240

Qy   81 TyrGlnProAspMetValAlaGlyValGlyTyrSerLeuGlyTyrSerAlaLeuValAlaSer   100
Db 241 TATCAGCCTGATATGGTTGCTGGTGTTGTCTTTGGAGAATACTCGCCTTGGTTGGCAAGC   300

Qy 101 GlyAlaLeuAspPheGluAspAlaAspSerGlyIleLysLysLysAlaLeuAlaArgGlyValAlaTyrMetGlu   120
Db 301 GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCCTAAGCGTGGAGCCTATATGAA   360

Qy 121 GluAlaAlaProAlaAspSerGlyLysLysMetValAlaAlaValLeuAsnThrProValGluVal   140
Db 361 GAAGCGGCTCCTGCTGACTCCGGCAAGATGGTGGCAGCAGTTCTCAATACGCCAGTAGAGGTC   420

Qy 141 IleGluGluAlaCysGlnLysLysAlaSerGluLeuGlyValValThrProAlaAsnTyrAsn   160
Db 421 ATTGAAGAAGCCTGTCAAAAAGCTTCGAACTTGGAGTGGTTACTCCAGCCAACTATAAC   480

Qy 161 ThrProAlaGlnIleValIleAlaGlyGluValAlaValAlaAspArgAlaValGluLeu   180
Db 481 ACACCTGCACAAATCGTCATTGCTGGAGAGGTTGCAGTCGCGGTTGAACTT   540

Qy 181 LeuGlnGluLeuAlaGlyAlaLysArgLeuIleProLeuLysValSerGlyValProHisThr   200
Db 541 TTGCAAGAGCAGGTGCCAAAGCGTTGATTCCTCTTAAGGTGTCAGGTCCCTTTCACC   600

Qy 201 AlaLeuGluLeuProAlaSerGlnLysLeuAlaGlyLeuThrLeuAlaGlnGlnValSerPheSer   220
Db 601 GCTCTCCTTGGACCCTGCTAGCCAGACTAGCTGAAACTCTAGCTCAGTTAAGTTTTTCA   660

Qy 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaAlaValMetGlnLysGluAspIle   240
Db 661 GATTTTACTTGCCCCCTAGTCGGCAATACGGAAGAAGCTGCTCGTGATGCAAAAGAGGACATT   720

Qy 241 AlaGlnLeuLeuThrArgGlnInValLysGluProLeuValArgPheTyrGluSerIleGlyVal   260
Db 721 GCTCAGCTCTTGACCGCGTCAGGTCAAGGAACCCGGTCGTTTCGTTCTATGAAAGTATTGGGGTC   780

Qy 261 MetGlnLeuAlaGlyIleSerAsnPheIleGluIleGlyLysProGlyLysValLeuSerGly   280
Db 781 ATGCAAGAGCAGCGGCATAAGCAACTTTATCGAGATTGGACCGGGGAAAGTTTGTCAGGT   840

Qy 281 PheValLysLysLysIleAspGlnInThrAlaHisLeuAlaHisLeuAlaSerLeu   300
Db 841 TTTGTTAAAAAATTGATCGAACTGCTCACTTAGCTCATGTGGAAGATCAAGGCGAGTTTA   900

Qy 301 ValAlaLeuLeuGluLys 306
Db 901 GTAGCACTTTTAGAAAAA 918

```
Pred. No.:                              9753
Score:                      6.91e-140   Matches:        305
Percent Similarity:         1514.00     Conservative:     1
Best Local Similarity:      100.00%     Mismatches:       1
Query Match:                99.67%      Indels:           0
DB:                         99.74%      Gaps:             0
                            50

US-09-308-397-2 (1-306) x US-60-068-175-555 (1-9753)

Qy      1 MetThrLysThrAlaPheLeuPheAlaGlyAlaGlnTyrLeuGlyMetGlyArg 20
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 ATGACTAAAACAGCCTTTTTATTTGCTGGTGCAAGTGCCCAGTATCTAGGGATGGGACGG 1293

Qy     21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1294 GATTTCTATGATCAGTATCCGATTGTCAAAGAAACGATTGATCGAGCGAGTCAGTGCTA 1353

Qy     41 GlyTyrAspLeuArgTyrLeuIleAspThrGluAspLysLeuAsnGlnThrArgTyr 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1354 GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGGACAAACTCAATCAGACCCGCTAT 1413

Qy     61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnLeuLysGly 80
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1414 ACGCAACCAGCCATCCTAGCGACTTCGGTTGCAATCTACCGTTTATTGCAAGAAAAGGGC 1473

Qy     81 TyrGlnProAspMetValAlaGlyTyrLeuGlyTyrSerAlaLeuValAlaSer 100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1474 TATCAGCCTGATATGGTTGCTGGTTATCTTGGTTGTTCCTTGGAGAATACTCTGCCTTGGTGTGGCAAGC 1533

Qy    101 GlyAlaLeuAspPheGluAlaSerGlyLysMetValAlaValAlaLeuAlaLeuAlaTyrMetGlu 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1534 GGCGCCCTGGATTTTGAAGATGCGGGTGCCTTGGTAGCTGAAGCCTATATGGAA 1593

Qy    121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValAlaLeuAsnThrProValGluVal 140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1594 GAAGCGGCAGAATCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 1653

Qy    141 IleGluValAlaCysGlnLysAlaSerGlnLeuGlyValValThrProAlaAsnTyrAsn 160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1654 ATTGAAGAAGCCTGTCAAAAAGCTTCGACTTGGAGTGGTTACTCCAGCCAACTATAAC 1713

Qy    161 ThrProAlaGlnIleValIleAlaGlyGluValAlaAspArgAlaValAlaGluLeu 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1714 ACACCTGCACAAATCGTCATTGCTGGAGAAGTGGTTGCAGTTGATCGAGCGGTTGAACTT 1773

Qy    181 LeuGlnGluAlaGlyAlaValLysArgLeuIleProLeuValSerGlyProPheHisThr 200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1774 TTGCAAGAAGCAGGTGCCAAACGCTTGATTCCTTTAAGTGTCAGGTCCCTTTCACACC 1833

Qy    201 AlaLeuGluProAlaSerGlnGlnLysLeuAlaGlnThrLeuAlaGlnValSerPheSer 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1834 GCTCTCCTTGAACCTGCTAGCCAGAAACTAGCTCAAACTCTGAAACCTCAGGTAAGTTTTTCA 1893

Qy    221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1894 GATTTTACTTGTCCCCTAGTGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT 1953

Qy    241 AlaGlnIleLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1954 GCTCAGATCCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC 2013

Qy    261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValSerGly 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2014 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAATTTGAAGGTGGGGAAAGTTTGTCAGGT 2073

Qy    281 PheValLysIleAspProGlnThrAlaHisLeuAlaGluValGlnAlaSerLeu 300
          ||||||||||||||::::::|||||||||||||||||||||||||||||||||
Db   2074 TTTGTTAAAAAATTGATCGAACTGCTCACTTAGCTGAAGTGCGGAAGATCAAGCAGGAGTTTA 2133

Qy    301 ValAlaLeuGluLys 306
          |||||||||||||||
Db   2134 GTAGCACTTTTAGAAAAA 2151
```

```
Qy    201 AlaLeuGluProAlaSerGlnLysLeuAlaGlnThrLeuAlaGlnValSerPheSer 220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCTCTCCTTGAACCTGCTAGCCAGAAACTAGCTGAAACTCTGAAACTCAGGTAAGTTTTTCA 660

Qy    221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GATTTTACTTGTCCCCCCAGTGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACATT 720

Qy    241 AlaGlnIleLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVal 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GCTCAGTTCCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGTC 780

Qy    261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATGCAAGAAGCAGGCATAAGCAACTTTATCGAGATTGGACCCGGGAAAGTTTGTCAGGT 840

Qy    281 PheValLysIleAspProGlnThrAlaHisLeuAlaGluValGlnAlaSerLeu 300
          ||||||||||||||::::::|||||||||||||||||||||||||||||||||
Db    841 TTTGTTAAAAAATTGATCGAACTGCTCACTTAGCTGAAGATCAAGCAGGAGTTTA 900

Qy    301 ValAlaLeuGluLys 306
          |||||||||||||||
Db    901 GTAGCACTTTTAGAAAA 918
```

```
RESULT 13
US-60-068-175-555

; Sequence 555, Application US/60068175
GENERAL INFORMATION:
   APPLICANT: Lagace, Robert E.
   APPLICANT: Corley, Neil C.
   APPLICANT: Russo, Frank D.
   APPLICANT: Hann, Amy L.
   APPLICANT: Heath, Joe D.
   APPLICANT: Finney, Gregory L.
   TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
   TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
   NUMBER OF SEQUENCES: 1175
   CORRESPONDENCE ADDRESS:
     ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
     STREET: 3174 PORTER DRIVE
     CITY: PALO ALTO
     STATE: CALIFORNIA
     COUNTRY: USA
     ZIP: 94304
   COMPUTER READABLE FORM:
     MEDIUM TYPE: Floppy disk
     COMPUTER: IBM PC compatible
     OPERATING SYSTEM: PC-DOS/MS-DOS
     SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
   CURRENT APPLICATION DATA:
     APPLICATION NUMBER: US/60/068,175
     FILING DATE: HEREWITH
     CLASSIFICATION:
   ATTORNEY/AGENT INFORMATION:
     NAME: CERRONE, MICHAEL C.
     REGISTRATION NUMBER: 39,132
     REFERENCE/DOCKET NUMBER: PM-0009-2 P
   TELECOMMUNICATION INFORMATION:
     TELEPHONE: (650) 855-0555
     TELEFAX: (650) 845-416
INFORMATION FOR SEQ ID NO: 555:
   SEQUENCE CHARACTERISTICS:
     LENGTH: 9753 base pairs
     TYPE: nucleic acid
     STRANDEDNESS: double
     TOPOLOGY: circular
   MOLECULE TYPE: genomic DNA
   IMMEDIATE SOURCE:
     CLONE: SPN2c557
US-60-068-175-555

Alignment Scores:
```

RESULT 14
US-60-061-998-494
; Sequence 494, Application US/60061998
; GENERAL INFORMATION:
; APPLICANT: LAGACE, ROBERT E.
; APPLICANT: CORLEY, NEIL C.
; APPLICANT: RUSSO, FRANK D.
; APPLICANT: HANN, AMY L.
; APPLICANT: HEATH, JOE D.
; APPLICANT: FINNEY, GREGORY L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
; TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
; NUMBER OF SEQUENCES: 797
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/061,998
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: CERRONE, MICHAEL C.
; REGISTRATION NUMBER: 39,112
; REFERENCE/DOCKET NUMBER: PM-0006-2P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 494:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5963 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; CLONE: SPN1c499
US-60-061-998-494

Alignment Scores:
Pred. No.:
Score: 1.5e-137   Length: 5963
                        1488.00   Matches: 302
Percent Similarity: 99.67%   Conservative: 1
Best Local Similarity: 99.34%   Mismatches: 0
Query Match: 98.02%   Indels: 1
DB: 50   Gaps: 0

US-09-308-397-2 (1-306) x US-60-061-998-494 (1-5963)

Qy   1 MetThrLysThrAlaPheLeuPheLeuAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg   20
Db 2919 ATGACTAAAAACAGCCTTTTTATTTGCTGTGGTCAAGGTGCCCAGTATCTAGGGATGGGACGG 2978

Qy   21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspAlaSerArgAlaSerGlnValLeu   40
Db 2979 GATTTCTATGATCAGTATCCGATTGTAAAGAAACGATTGATCGAGCGAGTCAGGTGCTA 3038

Qy   41 GlyTyrAspLeuArgTyrLeuIleAspThrGluAspAspLysLeuAsnGlnThrArgTyr   60
Db 3039 GGTTATGATTTGCGTTATCTCATCGATACGGAAGAGAAGAAACTCAATCAGACCCGCTAT 3098

Qy   61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLysGly   80
Db 3099 ACGCAACCAGCCATTCTAGCGACTTCGGTTGCTATCTACCGTTTATTGCAAGAAAAGGGC 3158

Qy   81 TyrGlnProAspMetValAlaAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer 100
Db 3159 TATCAGCCTGATATGGTGCTGCTGGTTGTCTTGTCTCTTGGAGAATACTCTGCCTTGGTGGCAAGC 3218

Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLeuLysArgGlyAlaThrTyrMetGlu 120
Db 3219 GGCGCCTTGGATTTTGAAGATGCGGTTGCCTTGGTAGCTAAGCGTGGAGCCTATATGGAA 3278

Qy 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuValAsnThrProValGluVal 140
Db 3279 GAAGCGGCTCCTGCTGACTCTGGCAAGATGGTAGCAGTTCTCAATACGCCAGTAGAGGTC 3338

Qy 141 IleGluGluAlaCysGlnLysAlaSerGlnLeuGlyValValThrProAlaAsnTyrAsn 160
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Qy 161 ThrPro-AlaGlnIleValIleAlaGlyValAlaValAlaAspArgAlaValGluGlu 180
Db 3399 ACACCTGGCACAAATCGTCATTGCTGGAGTGGTTGCAGTTGCTGATCGAGCGGTTGAACT 3458

Qy 180 uLeuGlnGluAlaGlyArgLeuIleProLeuLysValGlyProPheHisTh 200
Db 3459 TTTGCAAGAAGCAGGTGCCAAAGCCTTGATCCCTCTTAAGGTGTCAGGTCCCTTTCACAC 3518

Qy 200 rAlaLeuLeuGluProAlaSerGlnLysLeuAlaGluThrLeuAlaGlnValSerPheSe 220
Db 3519 CTCTCTCCTTGAACCTGCTAGCCAGAAACTAGCTGAAACTCTGGCTCAGGTAAGTTTTTC 3578

Qy 220 rAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIl 240
Db 3579 AGATTTTACTTGTCCCCTAGTCGGCAATACAGAAGCTGCTGTGATGCAAAAAGAGGACAT 3638

Qy 240 eAlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyVa 260
Db 3639 TGCTCAGCTCTTGACGCGTCAGGTCAAGGAACCCGTTCGTTTCTATGAAAGTATTGGGGT 3698

Qy 260 lMetGlnGluAlaGlyIleSerAsnPheIleGlyIleGlyProGlyLysValLeuSerGl 280
Db 3699 CATGCAAGAAGCAGGCATAAGCAACTTATCGAGATTGGACGGGGGAAAGTCTTGTCAGG 3758

Qy 280 yPheValLysIleAspSerGlnThrAlaHisLeuAlaHisValGluAspSerGlnAlaSerLe 300
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Qy 300 uValAlaLeu 303
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RESULT 15
US-60-360-039-42057
; Sequence 42057, Application US/60360039
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Chen, Xianfeng
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)A
; CURRENT APPLICATION NUMBER: US/60/360,039
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 42057
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Lactococcus lactis
US-60-360-039-42057

Alignment Scores:
Pred. No.:   Length: 927
Score: 1.53e-94   Matches: 208
                        1048.00   Conservative: 40
Percent Similarity: 80.52%

Best Local Similarity: 67.53%   Mismatches: 58
Query Match: 69.04%   Indels: 2
DB: 80   Gaps: 1

US-09-308-397-2 (1-306) x US-60-360-039-42057 (1-927)

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Qy    21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu  40
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Qy   121 GluAlaAlaAlaProAlaAspSerGlyLysMetValAlaLeuAlaValLeuAsnThrProValGluVal  140
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Db   361 GAAGCTGCACCCGACTGGTTCTGGTAAAATGGTCGCTGTAATGACAACAGACCCAGCCTTG  420

Qy   141 IleGluGluAlaCysGlnLysGlnLysAlaSerGluLeu------GlyValValThrProAlaAsn  158
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Db   421 ATTGAAGAAGCTTGCCAGAAGCGGCGAATTTAAAGGCGGTTATGTGAGTCCAGCAAAT  480

Qy   159 TyrAsnThrProAlaGlnIleValIleLeuValAlaGlyAlaValValValAlaValAspArgAlaVal  178
           ||| ||| ||||||:::||| |||||| |||||| ||||| |||||| |||||
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Db   541 GAGTTGCTAAAAGAAGCCGGAGTTCGTAAACTTATTGGTAAAACTTATTAAAAGTTTCAGGACCTTTC  600

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Db   721 GAAGTCAAAGGACTTTTGACCCGTCAAGTCATGAACCAGTTCGTTTTTATGAATCGGTT  780

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Db   781 GAAACAATGCAAAAACTAGGGGCAGCTCGCTTATTGAAGTGGTCCTGGGAGAGTACTT  840

Qy   279 SerGlyPheValLysIleAspGlnThrAlaHisLeuAlaHisGluValGluAspGlnAla  298
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Db   901 TCATTTGAAGCTTTGATTAATCAG  924
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          GenCore version 5.1.6
          Copyright (c) 1993 - 2003  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:   June 11, 2003, 20:37:43 ; Search time 660 Seconds
                                     (without alignments)
                         3077.862 Million cell updates/sec

Title:          US-09-308-397-2
Perfect score:  1518
Sequence:       1 MTKTAFLFAGQGAQYLGMGR........QTAHLAHVEDQASLVALLEK 306

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       7602234 seqs, 3319262570 residues

Total number of hits satisfying chosen parameters:     15204468

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09308397/runat_06062003_112350_28959/app_query.fasta_1.455
-DB=Pending_Patents_NA_New -QFMT=fastap -SUFFIX=rrpn -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09308397 @CGN_1_1_638 @runat_06062003_112350_28959 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=5 -DELOP=6 -DELEXT=7

Database :  Pending_Patents_NA_New:*
            1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
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           11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	1515	99.8	921	9	US-10-282-122A-37621		Sequence 37621, A
2	1108	73.0	918	9	US-10-282-122A-36004		Sequence 36004, A
3	1048	69.0	927	8	US-10-369-493-42057		Sequence 42057, A
4	1036	68.2	939	9	US-10-282-122A-38525		Sequence 38525, A
5	952	62.7	915	9	US-10-282-122A-21491		Sequence 21491, A
6	948	62.5	987	8	US-10-417-884-3319		Sequence 3319, Ap
7	937	61.7	927	9	US-10-282-122A-20712		Sequence 20712, A
8	937	61.7			US-09-134-000C-1582	948 6	Sequence 1582, Ap
9	937	61.7			US-09-134-000C-1582	948 9	Sequence 1582, Ap
10	937	61.7			US-10-434-665-1582	948 8	Sequence 1582, Ap
11	710.5	46.8			US-10-282-122A-15949	927 9	Sequence 15949, A
12	669.5	44.1			US-10-369-493-46809	954 9	Sequence 46809, A
13	657.5	43.3			US-10-282-122A-41191	939 9	Sequence 41191, A
14	654	43.1			US-10-369-493-41012	942 8	Sequence 41012, A
15	649.5	42.8			US-10-282-122A-32186	930 9	Sequence 32186, A
16	647	42.6			US-10-282-122A-16221	954 9	Sequence 16221, A
17	646	42.6			US-10-369-493-42861	918 8	Sequence 42861, A
18	643.5	42.4			US-10-369-493-24480	930 9	Sequence 24480, A
19	643.5	42.4			US-10-282-122A-20335	930 9	Sequence 20335, A
20	636	41.9			US-10-282-122A-21907	939 9	Sequence 21907, A
21 c	636	41.9	1830121		US-08-487-429B-1	1830121 4	Sequence 1, Appli
22 c	636	41.9	1830121		US-10-329-960-1	1830121 9	Sequence 1, Appli
23	628.5	41.4			US-10-282-122A-42230	930 9	Sequence 42230, A
24	626	41.2			US-10-282-122A-31257	939 9	Sequence 31257, A
25 c	619	40.8			US-10-194-163A-1003	9686 8	Sequence 1003, Ap
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27	616.5	40.6			US-10-282-122A-38967	930 9	Sequence 38967, A
28	612.5	40.3			US-10-282-122A-39704	930 9	Sequence 39704, A
29	610	40.2			US-10-282-122A-25339	945 9	Sequence 25339, A
30 c	608.5	40.1			US-60-453-134-364	2810 10	Sequence 364, App
31	602.5	39.7			US-10-282-122A-31669	1092 9	Sequence 31669, A
32	598.5	39.4			US-10-282-122A-23167	926 9	Sequence 23167, A
33	595	39.2			US-10-282-122A-36638	930 9	Sequence 36638, A
34	594.5	39.2			US-10-369-493-23749	981 8	Sequence 23749, A
35	593	39.1			US-10-369-493-30749	918 9	Sequence 30749, A
36	593	39.1			US-10-282-122A-12898	933 9	Sequence 12898, A
37	590	38.9			US-10-282-122A-13783	930 9	Sequence 13783, A
38	589.5	38.8			US-10-398-221-3519	2301 8	Sequence 3519, Ap
39	589	38.8			US-10-369-493-33689	945 8	Sequence 33689, A
40	588.5	38.8			US-10-282-122A-24478	942 7	Sequence 24478, A
41	586	38.6	319630		US-10-398-221-7	319630 8	Sequence 7, Appli
42 c	586	38.6	3011208		US-10-398-221-2058	3011208 8	Sequence 2058, Ap
43	584	38.5			US-10-369-493-32211	918 8	Sequence 3221, A
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45	582	38.3			US-10-369-493-27993	891 8	Sequence 27993, A

ALIGNMENTS

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RESULT 1
US-10-282-122A-37621
; Sequence 37621, Application US/10282122A
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT: Zamudio, Carlos
;  APPLICANT: Malone, Cheryl
;  APPLICANT: Haselbeck, Robert
;  APPLICANT: Ohlsen, Kari
;  APPLICANT: Zyskind, Judith
;  APPLICANT: Wall, Daniel
;  APPLICANT: Trawick, John
;  APPLICANT: Carr, Grant
;  APPLICANT: Yamamoto, Robert
;  APPLICANT: Forsyth, R.
;  APPLICANT: Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
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;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 37621
;  LENGTH: 921
;  TYPE: DNA
;  ORGANISM: Streptococcus pneumoniae
US-10-282-122A-37621

Alignment Scores:
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Score:                      1.93e-144         Matches:         305
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Best Local Similarity:      100.00%           Mismatches:        0
Query Match:                99.67%            Indels:            0
DB:                         99.80%            Gaps:              0

US-09-308-397-2 (1-306) x US-10-282-122A-37621 (1-921)
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;   APPLICANT:  Cao, Yongwei
;   APPLICANT:  Hinkle, Gregory J.
;   APPLICANT:  Slater, Steven C.
;   APPLICANT:  Goldman, Barry S.
;   APPLICANT:  Chen, Xianfeng
;   TITLE OF INVENTION:  EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
;   TITLE OF INVENTION:  PLANTS WITH IMPROVED PROPERTIES
;   FILE REFERENCE:  38-10(52052)B
;   CURRENT APPLICATION NUMBER:  US/10/369,493
;   CURRENT FILING DATE:  2003-02-28
;   PRIOR APPLICATION NUMBER:  US 60/360,039
;   PRIOR FILING DATE:  2002-02-21
;   NUMBER OF SEQ ID NOS:  47374
;   SEQ ID NO 42057
;       LENGTH:  927
;       TYPE:  DNA
;       ORGANISM:  Lactococcus lactis
US-10-369-493-42057

Alignment Scores:
Pred. No.:                                    Length:            927
Score:                       7.12e-97         Matches:           208
Percent Similarity:          1048.00          Conservative:       40
Best Local Similarity:       80.52%           Mismatches:         58
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US-09-308-397-2 (1-306) x US-10-369-493-42057 (1-927)

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Qy   21  AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu   40
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Db   61  GATTTGTATGAAATTACCCAGTTGTCAAAGACAGACTTTTAAAACCGCTCATTCAATTTTG   120

Qy   41  GlyTyrAspLeuArgTyrLeuIleGluAspThrGluLysLeuAsnGlnThrArgTyr      60
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Db  121  GGATATGATCTTCGTGCTTTGATTGATGAAATGAAGAAAACTAAATCAAACACGTTAT    180

Qy   61  ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnLeuLysGly   80
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Db  481  ACTCCAGCACAAATTGTTATTGCTGGTGTTGAAGTAGCAGCTGTTGCTGATAGAGCTGT   540

Qy  181  LeuGlnLeuAlaGlyLeuAlaLysArgArgLeuIleLeuProLeuLysSerValSerGlyProPheHisThr  200
         |||||:       :|||||:||||
Db  541  TTAAAGGGAGCCACCGCTGGAGTGGGTAAGCTTGATTTCTGTTCTTAAAGTTTCTGGTCCCTTTCATACG   600

Qy  201  AlaLeuLeuAsnLeuLysAlaSerGlnIleLysLeuAlaGluThrLeuAlaGlnValSerPheSer  220
         |||:||        ::|:
Db  601  GCTCTTTTTGAAATCTGCTAGTCAAGCTTGGCTCAAGCTTTGGAAAATATTAAATTTTCA   660

Qy  221  AspPheThrArgProLeuValGlyTyrAsnThrGluAlaAlaValMetGlnLysGlyGluAspIle  240
         ||||         :|||:|
Db  661  GATTTCATCCTTCCACTAGTGGGGAACACTGAAATTATGAAGAAGCAACAGGAGATT   720

Qy  241  AlaGlnLeuLeuThrArgAspPheValGluProAlaArgPheTyrArgLysTyrProGlyIleGluGlyVal  260
         |||:||       |||:|||:|
Db  721  AAACCTTTGCTTGCCTGCGTCCAAGTCAAAGAACCTGTTGCTCGTCGTCATGAATCTATTGCGTGTA   780

Qy  261  MetGluAlaAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuuSerGly  280
         |||:         |:|:|:|:||
Db  781  ATGGAAGCAGCTGGTATCTCGAATTTGATTGAAATTGACCTGGTAAGGTCTTGAGTGGT   840

Qy  281  PheValLysLysIleAspGlnThrArgAlaHisValGluLeuAlaHisIleSerLeuAlaSerLeu  300
         |||||:       :||:|
Db  841  TTTGTGAAAAAGATTGATAAATCTCAGCTGTTGAAGAGATCTCAGCTGTTGAAGACTTAGCTAGTTTG   900

Qy  301  ValAlaLeuLeuGlu  305
         ||:||:
Db  901  CAGGCTTTCTTAGAT   915
```

RESULT 3
US-10-369-493-42057
; Sequence 42057, Application US/10369493
; GENERAL INFORMATION:

US-09-308-397-2 (1-306) x US-10-282-122A-36004 (1-918)

```
Qy    1  MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg   20
         ||||||||||||||||||||||||||
Db    1  ATGACAAAAACAGCATTTTTATTCGCGGCCAAGGAGCTCAAAAACTTGGTATGGCAAGT    60

Qy   21  AspPheTyrAspGlnTyrProIleValLysProValLeuValLysGluThrIleAspArgAlaSerGlnValValLeu   40
         ||||||:|||||||         :::|||
Db   61  GATTTGTATGAAATTTACCCAGTTCAAAGACAGACTTTTAAAACCGCTCATTCAATTTTG   120

Qy   41  GlyTyrAspLeuArgTyrLeuIleGluLeuLeuLysLeuAspGluLysLeuAsnGlnThrArgTyr   60
         ||:|||||||:|||        ::||
Db  121  GGATATGATCTTCGTGCTTTGATTGATGAAATGAAGAAAACTAAATCAAACACGTTAT   180

Qy   61  ThrGlnProAlaIleLeuGluLeuAlaThrSerValAlaIleAlaIleTyrArgLeuLeuGlnLeuLysGly   80
         ||:||||||||||:|||||||
Db  181  GCACAGCCAGCCGATTTTAACAACTTCAGTAGCTATTTATCGTCTTTTGAAAGAAAAGGT   240

Qy   81  TyrGlnProAspMetValAlaGlyLeuSerLeuGlyTyrGluTyrSerAlaLeuValAlaSer  100
         ||||||||||||||              :::
Db  241  TATCAACCAGACATTGTTGCTGGACTGTCACTAGGAGAAATACTCTGCTCTTGTTGCAGCC   300

Qy  101  GlyAlaLeuAspPheGluAspGluGluAlaTyrMetGlu  120
         ||||||              ::||
Db  301  GGTGCCATTTCAATTCAATTGAAGATGCCTTAGCCGTTGGTGTGAATTTATGGAA   360

Qy  121  GluAlaAlaProAlaAspSerGlyLysMetValAlaValAlaLeuAsnThrProValGlu   140
         |||             ||:|:|
Db  361  ACAGCAGCACCCGCTGGAGTGGGGAAAATGGTTGCTGTTGCTATTTACGTTGTTAAGTGAGAATGGGCTC   420

Qy  141  IleGluGluAlaCysGlnLysAlaSerGlnLysGlyValValThrProAlaAsnTyrAsn   160
         ||||||:        ::||||:
Db  421  ATTGAAGAAGATTGTCAGAAAGCCAGTGAAAAAGGCATTGTTACTCCAGCTAATTATAAT   480

Qy  161  ThrProAlaGlnIleValIleGlyValGluValAlaAlaValAlaAspArgAlaValGluLeu   180
         ||||:        ::||||
Db  481  ACTCCACACAAATTGTTATTGGTGGTGTTGAAGTAGCAGCTGTTGATATGCTGTGGAACTT   540

Qy  181  LeuGlnLeuAlaGlyAlaLysArgArgLeuIleLeuProLeuLysSerValSerGlyProPheHisThr   200
         |||:        :||:|||
Db  541  TTAAAGGGAGCCACCGCTGGAGTGGGTAAGCTTGATTTCTGTTCTTAAAGTTTCTGGTCCCTTTCATACG   600

Qy  201  AlaLeuLeuAsnLeuLysAlaSerGlnIleLysLeuAlaGluGlnValSerPheSer  220
         |||:        :::
Db  601  GCTCTTTTTGAAATCTGCTAGTCAAGCTTGGCTCAAGCTTTGGAAAATATTAAATTTTCA   660

Qy  221  AspPheThrArgProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGlyGluAspIle  240
         |||             :::
Db  661  GATTTCATCCTTCCACTAGTGGGGAACACTGAAATTATGAAGAAGCAACAGGAACAGGAGATT   720

Qy  241  AlaGlnLeuLeuThrArgAspPheValGluProAlaArgPheTyrArgLysTyrProGlyTyrGlyVal  260
         |||:        |||:|||:
Db  721  AAACCTTTGCTTGCCTGCGTCCAAGTCAAAGAACCTGTTGCTCGTCGTCATGAATCTATTGCGTGTA   780

Qy  261  MetGlnGluAlaAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuuSerGly  280
         |||:        :::
Db  781  ATGCAAAAATTTTGGTGAATACTATCGAAATTGGACCTGGTAAGGTCTTGAGTGGT   840

Qy  281  PheValLysLysIleAspGlnThrArgAlaHisIleSerLeuAlaHisValGluLeuGluAlaSerLeu  300
         |||||:        :|||:
Db  841  TTTGTGAAAAAGATTGATAAATCTCAGCTGTTGAAGAGATCTCAGCTGTTGAAGACTTAGCTAGTTTG   900

Qy  301  ValAlaLeuLeuGlu  305
         ||:||:
Db  901  CAGGCTTTCTTAGAT   915
```

Best Local Similarity: 68.30%   Mismatches: 58
Query Match: 68.25%   Indels: 0
DB: 9   Gaps: 0

US-09-308-397-2 (1-306) x US-10-282-122A-38525 (1-939)

Qy   1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg 20

Db   1 ATGACAAAGACAGCCTTTTATTTGCCGGTCAAGGTGCTCAAAAATTAGGGATGGGCAAGG 60

Qy 21 AspPheTyrAspGlnTyrProLeuValLysGluThrIleAspArgAlaSerGlnValLeu 40

Db 61 GATTTTTATGATAACTTTGCTATTGTGAAGAAAAACCTTTGATCAAGCTAGTCAAGTATTG 120

Qy 41 GlyTyrAspLeuArgTyrLeuGlyIleLeuAspThrGluGluAspLysLeuAsnGlnThrArgTyr 60

Db 121 GGATACGATTTGCGCGTTGATGATGTGACGAGTAAAACTTAATCAAACTAGCTAT 180

Qy 61 ThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnLysGly 80

Db 181 ACGCAACCAGCTATTTTGACATCATCAATTGCTATTTACCGTGTTTTGGGCTTACATCAC 240

Qy 81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluGlyTyrSerAlaLeuValAlaSer 100

Db 241 GTTAAACCGGATATGGTAGCTGGTCTTCCTTAGGAGAATACTCAGCTTGGTAGCATCA 300

Qy 101 GlyAlaLeuAspPheGluAspAlaValAlaLeuLysArgGlyAlaTyrMetGlu 120

Db 301 GGGGCACTCTCTTTGAAGATACCCTATCCTTAGTAGCTTAAGAGAGGCCGCTTGATGGAG 360

Qy 121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal 140

Db 361 GAAGCAGCACCAAAGGATCTGGAAAAGATGGTTGCCGTTATGAATACAGACGTGCAAGTC 420

Qy 141 IleGluGluAlaCysGlnLysAlaSerGlnLeuGlyValValThrProAlaAsnTyrAsn 160

Db 421 ATCGAAGAAGTCTGTCAAATAGCTGCTAAACATGAGTGGTTGCTCCAGCAAACTATAT 480

Qy 161 ThrProAlaGlnIleValIleValAlaGlyGluValValAlaValAlaAspArgAlaValGluLeu 180

Db 481 ACTCCTAGTCAAATTGTAATTGTGGTCAGACAGATGCTGTGAACGTGGCAGTTGAACTT 540

Qy 181 LeuGlnLeuAlaGlyLysArgLeuIleProLeuLysValSerGlyProPheHisThr 200

Db 541 TTAAAGGAAGGGGAGTTAAGCGTTTAATCCCTTAAACGTGTCAGGTCCTTTCCACACT 600

Qy 201 AlaLeuLeuGluProAlaSerGlnLysLeuLeuAlaGluThrLeuAlaGlnValSerPheSer 220

Db 601 GCTTTGTTAGAACCAGCTAGCCGCTTGTTGGCTAAAGAGTTGGAAAGATACAACTTCAGT 660

Qy 221 AspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIle 240

Db 661 GACTTCAAGATTCCTTTGGTTGGTAATACCGAAGCTAATATTATGGAAAAAGACCGTATC 720

Qy 241 AlaGlnLeuLeuThrArgGlnValLysGluProValArgPheGluSerIleGlyVal 260

Db 721 CCAGAACTATTAGCCCGTCAAGTCAAGGCCGTTCGTTTTATGACAGTGTTGCGACT 780

Qy 261 MetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGly 280

Db 781 TTAGTAGAAGTGGCATAACAATTCATTGAGTGAGGTAGGACCAGGTAAGGTTTGACAGGT 840

Qy 281 PheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAlaGlnAlaSerLeu 300

Db 841 TTTGTGAAGAAAATTGATAAAAATTTACTATGTACTAGTGTTGAAAACATGGTAAGCTTA 900

Qy 301 ValAlaLeuGluGluLys 306

Db 901 CGTTTATTTTTAGATAGA 918

RESULT 5
US-10-282-122A-21491
; Sequence 21491, Application US/10282122A

Qy 219 PheSerAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGlu 238

Db 661 TTTAGACCTTTTGAATTACCATTAATCTCAAATACGAGTGCTAAAGTAATGGAAAATGAT 720

Qy 239 AspIleAlaGlnLeuLeuThrArgGlnValLysGluProValArgPheGluSerIle 258

Db 721 GAAGTCAAAGACCTTTTGACGCGTCAAGTCATGGAACCAGTTCGTTTTTCGTTTTTGAATCGGTT 780

Qy 259 GlyValMetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeu 278

Db 781 GAAACAATGCAAAAACTAGGGGCGACTCGCTTTATTGAAGTTGGTCCTGGGAGAGTACTT 840

Qy 279 SerGlyPheValLysIleAspGlnThrAlaHisLeuAlaHisValGluAlaGlnAla 298

Db 841 TCAGGTTTCATTAAAAAAATTGATAAAAATGCAGAAAATTGCTAATGTTGAAAATTTAGCT 900

Qy 299 SerLeuValAlaLeuGluGluLys 306

Db 901 TCATTTGAAGCTTTGATTAATCAG 924

RESULT 4
US-10-282-122A-38525
; Sequence 38525, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang,Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38525
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-10-282-122A-38525

Alignment Scores:
Pred. No.:   1.21e-95   Length: 939
Score: 1036.00   Matches: 209
Percent Similarity: 81.05%   Conservative: 39

```
Db  241 CCAGATGCAGCTTGTTTAGGACTGAGTTTAGGAGAATTATTCGGCATTAGTAGCTAGTAATGCG 300
        |||||                  |||||||||||||||||||||||||||||||||||||||||||||
Qy  103 LeuAspPheGluArgThrGluValAlaLeuValAlaLeuLysArgGlyAlaTyrMetGluGluAla 122
        ||   ::::::         :::::|||||||
Db  301 CTATCCTTCACTGAAGCAGTTGCCTTAGTAGCAAAAAGAGGCGCTTATATGACAGAAGCT 360

Qy  123 AlaProAlaAspSerGlyLysMetValAlaValAlaValLeuAsnThrProValGluValIleGlu 142
        |||||||||::::   |||||||||||||||::::::|||||||
Db  361 GCCCCAGCTGGAAATGTTGCAGTGATGATGAATGAAACGATCGAG 420

Qy  143 GluAlaCysGlnLysValAlaSerGluLeuGlyValValThrProAlaAsnTyrArgAsnThrPro 162
        :::::::   :::|||
Db  421 GAAAGCTGTCATGAAGCTAGCAAGTACGGGCATCCTCTGCAAATTATAATTACACCT 480

Qy  163 AlaGlnIleValIleValIleAlaGlyGluValAlaValAlaValAspArgAlaValGluLeuLeuGln 182
        ||||||:::|||
Db  481 CAGCAGATCGTGATTGGTGGCGAAGAAAAGCAGTAGACGAAGCTGTTTTACTATTAAAA 540

Qy  183 GluAlaGlyAlaLysArgLeuLeuProLeuLysValSerGlyProPheHisThrAlaLeu 202
        :::|||||||:::
Db  541 GAAAAAGGGTTCAAAAGAATGATCCCTCTAAATGTCAGCGGGCCTTTTCATACAGCTATT 600

Qy  203 LeuGluProAlaSerGlnLysLeuLeuAlaGluThrLeuAlaGlnValSerPheSerAspPhe 222
        :::|||||:::||
Db  601 TTAGAACCGGCAGCAAAAAAACTGGCAGAAGGACCTAAGTCAGATTCAATTCTCTGAACCT 660

Qy  223 ThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIleAlaGln 242
        ::: :::::: :::
Db  661 TCTTTTCCATCATAAGCACACAACACGAAATAATGAAGAAAGAAGAAACAATCGCGGGA 720

Qy  243 LeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyValMetGln 262
        |||||        :::|||||
Db  721 CTACTTGAACAGCAAGTCATGCAACCTGTTCGTTTCTATGAGAGTATCCATAAGTTAAAA 780

Qy  263 GluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGlyPheVal 282
        :::        ||||||
Db  781 ACAATCGCATCGACAAGTCATCGAAGCGTCGGCCCCGGAAAGATTAAGCGGATTTATG 840

Qy  283 LysLysIleLeuAspGlnThrArgAlaHisLeuAlaHisValGlyLeuAspGlnAlaSerLeu----- 300
        :::||||||      :::  :::
Db  841 AAAAAAATCGATAAAACAATACCAGTTCTGCGTGTTGAGAATAAGCAGACATTTGATGAA 900

Qy  301 ---ValAlaLeuLeu 304
        ::|||
Db  901 ACAATAGCAATACTA 915
```

RESULT 6
US-10-417-884-3319
Sequence 3319, Application US/10417884

```
Alignment Scores:
Pred. No.:                    4.19e-87          Length:        915
Score:                        952.00            Matches:       189
Percent Similarity:           78.36%            Conservative:  50
Best Local Similarity:        61.97%            Mismatches:    62
Query Match:                  62.71%            Indels:        4
DB:   915                                       Gaps:          2

US-09-308-397-2 (1-306) x US-10-282-122A-21491 (1-915)

Qy    3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArgAspPhe 22
        |   |||||||||||||||||||||||::::||||| |||||:::
Db    4 AAAACAGCATTCTTATTTAGTGCCAAGGTGCACAATATCAAGGTATGGGAAAAAGATTTA 63

Qy   23 TyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeuGlyTyr 42
        |||::::::      :::::||||||||||||||:::::|||||
Db   64 TACTGAAGAA---GCCGTTGTAAAGCAGACAATTTGATGAAGCAGTGAGATTCTCGGCTAC 120

Qy   43 AspLeuArgThrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyrThrGln 62
        ||||||:::|:::|||||||||::::|||||||||:::|||
Db  121 GATATGGCTGAACTTGCTTGACCATCGAGAAAATGAACGTTGGATCAGACGCAATATACACAG 180

Qy   63 ProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLeuLysGlyTyrGln 82
        ||||||        |||:::::||||||  :::|||
Db  181 CCAGCTATTCTAACAGTCAGCATCGCGTATTATCGGCTATTGAAGGAGCCATTGAATCATC 240

Qy   83 ProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaLeuAlaSerGlyAla 102
        ||||||
```

APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
  NAME: Ariniello, Pamela Deneke
  REGISTRATION NUMBER: 40,489
  REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (781)893-5007
  TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3319:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 987 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: double
    TOPOLOGY: circular
  MOLECULE TYPE: DNA (genomic)
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
  ORIGINAL SOURCE:
    ORGANISM: Enterococcus faecium
  FEATURE:
    NAME/KEY: misc_feature
    LOCATION: (B) LOCATION 1...987
  SEQUENCE DESCRIPTION: SEQ ID NO: 3319:
US-10-417-884-3319

Alignment Scores:
Pred. No.:   1.18e-86   Length: 987
Score: 948.00   Matches: 188
Percent Similarity: 78.03%   Conservative: 50
Best Local Similarity: 61.64%   Mismatches: 63
Query Match: 62.45%   Indels: 4
DB: 8   Gaps: 2

US-09-308-397-2 (1-306) x US-10-417-884-3319 (1-987)

```
Qy     3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArgAspPhe  22
           |||:||::||||: |||:|  ::::|:|:  :|::
Db    73 AAAACAGCATTCTTATTAGTGGCCAAGGTGCACAATATCAAGGTATGGGAAAAGATTTA 132

Qy    23 TyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeuGlyTyr  42
           ||:||:||     ||||:|| :||||||  |:::| : ::::|
Db   133 TATGAAGAA--GCCGTTGTAAAGCAGACATTTGATGAGCAAGTGAGATTCTCCGGCTAC 189

Qy    43 AspLeuArgTyrLeuIleAspThrGluAspLysLeuAsnGlnThrArgTyrThrGln  62
           ||:||   :  ::::::||| ::::||:|
Db   190 GATATCGGCTGAACTTTGCTTTACAGAAATGAACGTTTGGATCAGACGGCAATATACACAG 249

Qy    63 ProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGlnLysGlyTyrGln  82
           ::::|:|||||| |||:|::|:
Db   250 CCAGCTATTCTAACAGTCAACATCGCGTATTATCGCTTATTGAAGGAGCATGGAATCATC 309

Qy    83 ProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSerGlyAla 102
           |||||| | : ::: | : :||||||:|
Db   310 CCAGATGCAGCTTTAGGACTGAGTTTAGGAGAAATATTCGGCATTAGCTAGTAATGCG 369

Qy   103 LeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGluGluAla 122
           ::::::|
Db   370 CTATCCTTCACTGAAGCAGTTGCGTTAGTAGCAAAAGAGGCGCTTATATGACAGAAGCT 429

Qy   123 AlaProAlaAspSerGlyLysMetValAlaValAlaLeuAsnThrProValGluValIleGlu 142
           ::::| |||||||  ||::| |::| ::
Db   430 ACCCCAGCTGAAGCGGGAAAATGGTTGCAGTGAATGCGCCGATTGAAACAGATCGAG 489

Qy   143 GluAlaCysGlnLysAlaSerGluLeuGlyGlyValValThrProAlaAsnTyrAsnThrPro 162
           |:::::|:: ||: :: ::|||
Db   490 GAAAGCTGTCATGAAGCTAGCAAGTACGGCCATCGTATCCTGCAAATTATAATACACCT 549

Qy   163 AlaGlnIleValIleAlaGlyGlyValValAlaValAlaValAspArgArgAlaValGluLeuLeuGln 182
           :::|::: ::
Db   550 CAGCAGATCGTGATTGGTGGCGAAGAAAAAGCAGTAGACGAAGCTGTTTTTACTATTAAAA 609
```

183 GluAlaAlaAlaLysArgLeuIleProLeuLysValSerGlyTyrProPheHisThrAlaLeu 202
Qy
Db 610 GAAAAAGGGTTCAAAGAATGATCCCCTCTAAATGTCAGCGGCGCCTTTTCATACAGCTATT 669

203 LeuGluProAlaSerGlnLysGluLeuAlaGluThrLeuAlaGlnValSerPheSerAspPhe 222
Qy
Db 670 TTAGAACCGGCAGCAAAAAAACTGGCAGAGGACCTAGTCAGATTCAATTCTCTGAACCT 729

223 ThrCysProLeuValGlyTyrAsnThrGluAlaAlaValMetGlnLysGluAspIleAlaGln 242
Qy
Db 730 TCTTTTCCTATCATAAGCAACACAACAAGCGAAATAATGAAGAAAGAAACAATCGGCGGGA 789

243 LeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyValMetGln 262
Qy
Db 790 CTACTTGAACACGCAAGTCAACCTGTTCGTTTCGTTTCATGAGAGTATCCATAAGTTAAAA 849

263 GluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGlyPheVal 282
Qy
Db 850 ACAATCGGCATCGAACAAGTCATCGAAGTCGGCCCCCGAAAAGTATTAAGCGGATTTATG 909

283 LysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSerLeu------ 300
Qy
Db 910 AAAAAAATCGATAAAACAATACCAGTTCTGCGTGTTGAGAATAAGCAGACATTTGATGAA 969

301 --ValAlaLeuLeu 304
Qy
Db 970 ACAATAGCAATACTA 984

RESULT 7
US-10-282-122A-20712
; Sequence 20712, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20712

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; LENGTH: 927
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-20712

Alignment Scores:
Pred. No.:              1.44e-85        Length:         927
Score:                  937.00          Matches:        187
Percent Similarity:     75.17%          Conservative:   40
Best Local Similarity:  61.92%          Mismatches:     75
Query Match:            61.73%          Indels:         0
DB:                                     Gaps:           9

US-09-308-397-2 (1-306) x US-10-282-122A-20712 (1-927)

Qy    3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArgAspPhe  22
          ::: |||::::::||   |   |||::::     |::       :::
Db    4 AAAACAGCGATTTTATTTAGTGGACAAGGAGCCCAGTATCAAGGGATGGGTGAAGAATTA  63

Qy   23 TyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeuGlyTyr  42
          ||||||||    :::|||::::     ::: |||||||
Db   64 TATCACCAAGAAGCGATTGTTCGGGAAACTTTCGATGAAGCAAGTCATATCTTAGGTTAT 123

Qy   43 AspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyrThrGln  62
          ::::|||||||   |||:::
Db  124 GAGATGGCAGAACTTTGTTTTACTGAAAATGAAACGTTTAAATGAACAGAATATACGCAA 183

Qy   63 ProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGluGlnLysLysGlyTyrGln  82
          |||||||      |||:::|||::::   |||
Db  184 CCTGCTATTTTAACAGTCAGTGTCGCATTTTACCGTCTTTTGCAACAAAAAGGACTAACG 243

Qy   83 ProAspMetValAlaGlyLeuSerLeuGlyValGluTyrSerAlaLeuValAlaSerGlyAla 102
          ::::|||||||   ::::|||  |:::|||
Db  244 CCTGATGTCGTAGCGGGTTTAAGCTTAGGGGAATACAGTGCTTGGTGCCAGCGGGGGCT 303

Qy  103 LeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyTyrMetGluGluAla 122
          |||||||      |||:::|||
Db  304 TTGCGTTTCGAAGACGCTGGCCTTGGTCCAAAAGCGGGTCAGTACATGACAGAAGCA 363

Qy  123 AlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluValIleGlu 142
          |||||||      |||:::
Db  364 GCACCACAAGGACTGGCAAAATGGTTGCTGTTATGAATGGCGTGAAGTAATTGAG 423

Qy  143 GluAlaCysGlnLysAlaSerGlyLeuLeuGlyValValThrProValAlaAsnTyrAsnThrPro 162
          :::|||||||   ::::|||
Db  424 AAAGCCTGCCAAGAAGGCCAGTGCTTTCCGAATTGTGGCTCCAGCAAATTATATACACCA 483

Qy  163 AlaGlnIleValIleLeuAlaGlyLeuValValValAlaValAlaAspArgAlaValGluLeuLeuGln 182
          ||||||||:::||||||
Db  484 CAACAAATCGTGATTGGTGGTGAGGTTGCTGTCGTGTTGATCAAGCGATGACACTTCTCAAA 543

Qy  183 GluGluLeuProLeuAlaSerGlyIleLeuProLeuLysSerValSerGlyValSerGlyValProPheHisThrAlaLeu 202
          :::|||||||   ::::|||
Db  544 GAAGCTGGTGTGATGGAAGCGAATGATTCCGTTAAATGTGAGCGGTTAAGTGAGTAATTGGA 603

Qy  203 LeuGluProAlaSerGlnIleLeuAlaGlyThrLeuAlaGlnIleValSerPheSerAspPhe 222
          |||||||      |||:::
Db  604 TTACAACCAGCATCCAAAAAAAAATTGGCTCAGGATTTAGCAAATTGAACTTTCAAACCATG 663

Qy  223 ThrCysProLeuValGlyAlaAsnThrGluAlaAlaValMetGlnIleLysGlyLeuAspIleAlaGln 242
          :::|||||||   :::|||
Db  664 CAAATTCCTGTCATTAGTAATACGACTGCGAAATTATGCCCCAAGAGGCAATTCAAGCG 723

Qy  243 LeuLeuThrArgGlnIleLysGluTyrArgPheTyrGluSerIleGlyValMetGln 262
          |||||||      ::::|||
Db  724 TTATTGGAAAGCAAGTCATGTCGCGGTACGTTTGAAGACAGTATCGAAACGATGAAG 783

Qy  263 GluAlaGlyGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGlyPheVal 282
          |||||||      ::::|||
Db  784 GCTATGAACGTAGGAACGATGATTGAAGTTGGTCCAGGGAAAAACATTAACTGGTTTTTGTT 843

Qy  283 LysIleLysAspGlnIleThrAlaHisLeuAlaHisValGluHisAspGlnIleAlaSerValAla 302
          :::|||||||
Db  844 ... 903
```

```
Db  844 AAAAAAATTGACAAAACAATTGAAATGACCGTGTGGAAGAATGTTGCACATTAACAGAA 903

Qy  303 LeuLeu 304
          |||
Db  904 ACGTTA 909


RESULT 8
US-09-134-000C-1582
; Sequence 1582, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1582

Alignment Scores:
Pred. No.:              1.48e-85        Length:         948
Score:                  937.00          Matches:        187
Percent Similarity:     75.17%          Conservative:   40
Best Local Similarity:  61.92%          Mismatches:     75
Query Match:            61.73%          Indels:         0
DB:                                     Gaps:           6

US-09-308-397-2 (1-306) x US-09-134-000C-1582 (1-948)

Qy    3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArgAspPhe  22
          ::: |||:::
Db   22 AAAACAGCGATTTTATTTAGTGGACAAGGAGCCCAGTATCAAGGGATGGGTGAAGAATTA  81

Qy   23 TyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeuGlyTyr  42
          |||||||
Db   82 TATCACCAAGAAGCGATTGTTCGGGAAACTTTCGATGAAGCAAGTCATATCTTAGGTTAT 141

Qy   43 AspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyrThrGln  62
          ::::|||
Db  142 GAGATGGCAGAACTTTGTTTTACTGAAAATGAAACGTTTAAATGAACAGAATATACGCAA 201

Qy   63 ProAlaIleLeuAlaThrSerValAlaIleThrSerValAlaIleTyrArgLeuLeuGluGlnLysLysGlyTyrGln  82
          |||||||:::
Db  202 CCTGCTATTTTAACAGTCAGTGTCGCGATTTTACCGTCTTTTGCAACAAAAAGGACTAACG 261

Qy   83 ProAspMetValAlaGlyLeuSerLeuGlyValGluTyrSerAlaLeuValAlaSerGlyAla 102
          :::|||||||
Db  262 CCTGATGTCGTAGCGGGTTTAAGCTTAGGGGAATACAGTGCTTTGGTTGCCAGCGGGGGCT 321

Qy  103 LeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyTyrAlaTyrMetGluGluAla 122
          |||||||
Db  322 TTGCGTTTCGAAGACGCTGGCCTTGGTCCAAAAGCGGGTCAGTACATGACAGAAGCA 381

Qy  123 AlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluValIleGlu 142
          |||||||
Db  382 GCACCACAAGGACTGGCAAAATGGTTGCTGTTATGAATGGCGTGAAGTAATTGAG 441

Qy  143 GluAlaCysGlnLysAlaSerGlyLeuLeuGlyValValThrProValAlaThrProAlaAsnTyrAsnThrPro 162
          :::|||
Db  442 AAAGCCTGCCAAGAAGGCCAGTGCTTTCCGAATTGTGGCTCCAGCAAATTATATACACCA 501

Qy  163 AlaGlnIleValIleLeuAlaGlyLeuValValValAlaValAlaAspArgAlaValGluLeuLeuGln 182
          :::|||
Db  502 CAACAAATCGTGATTGGTGGTGAGGTTGCTGTCGTGTTGATCAAGCGATGACACTTCTCAAA 561

Qy  183 GluAlaGlyAlaAlaLysArgLeuIleLeuProLeuLysSerValSerGlyValSerGlyValProPheHisThrAlaLeu 202
          :::|||
Db  502 ...
```

Qy 83 ProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSerGlyAla 102
Db 262 CCTGATGTGTAGGCGGGTTAAGCTTGTTCTGTTAAATGTGAGTGGCCCTTTGGTGCCAGGGGCT 321

Qy 103 LeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyrMetGluGluAla 122
Db 322 TTGCGCTTTTCAGAAGCAGTGGCCTTGGTCAGAAATTGAACTTCAAACGATG 381

Qy 123 AlaProAlaAspSerGlyLysMetValAlaValAlaLeuAsnThrProValGluIleGlu 142
Db 382 GCACCACAAGGAACTGGCAAAATGATGCCGAAATTATGCCCAAGAGGCAATTCAAGCG 441

Qy 143 GluAlaCysGlnLysSerGlnLeuGlyValValThrProAlaAsnTyrAsnThrPro 162
Db 442 AAAGCCTGCCAAGAGCCAGTGCTTTCGAATTGTGGCTCCAGCAAATTATATACCA 501

Qy 163 AlaGlnIleValIleAlaGlyGlyValAlaValAlaAspArgAlaValGluLeuLeuGln 182
Db 502 CAACAAATCGTGATTGGTGGTGAGGTTGCTGCTGTTGGATCAAGCGATGACACTTCTCAAA 561

Qy 183 GluAlaGlyArgGlnLysValSerGlyProPheHisThrAlaLeu 202
Db 562 GAAGCTGGTGTGAAGCGAATGATTCCGTTAAATGTGAGTGGCCCTTTCCATACGGCGCTG 621

Qy 203 LeuGluProAlaSerGlnLysLeuAlaGlnThrLeuAlaAlaValMetGlnLysGluAspPhe 222
Db 622 TTACAACCAGCATCAAAAAAATTGGCTCAGGATTTAGCAAAATTGAACTTTCAAACGATG 681

Qy 223 ThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIleAlaGln 242
Db 682 CAAATTCCTGCTCATTAGTAATACGACTGCCGAAATTATGCCCAAGAGGCAATTCAAGCG 741

Qy 243 LeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyValMetGln 262
Db 742 TTATTGGAAAAGCAGTCATGTCTGCGGTACGTTTGAAGACAGTATCGAAACGATGAAG 801

Qy 263 GluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysValLeuSerGlyPheVal 282
Db 802 GCTATGACGTAGGAACCATGATTGAAGTTGGTCCAGGGAAAACATTAACTGGTTTTGTT 861

Qy 283 LysLysIleAspGlnThrAlaHisLeuAlaHisValGlnAspGlnAlaSerLeuValAla 302
Db 862 AAAAAAATTGACAAAACAATTGAAATGCACACCGTGTGGAAGATGTTGCACATTAACAGAA 921

Qy 303 LeuLeu 304
Db 922 ACGTTA 927

RESULT 10
US-10-434-665-1582
; Sequence 1582, Application US/10434665
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-09
; CURRENT APPLICATION NUMBER: US/10/434,665
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: US 09/134,000
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-434-665-1582

Alignment Scores:
Pred. No.:
Score: 1.48e-85
                                                 937.00
                                                 Length: 948
                                                 Matches: 187

Db 562 GAAGCTGGTGTGAAGCGGAATGATTCCGTTAAATGTGAGTGGCCCTTTCCATACGGCGCTG 621

Qy 203 LeuGluProAlaSerGlnLysLeuAlaGluLeuSerPheSerAspPhe 222
Db 622 TTACAACCAGCATCAAAAAAATTGGCTCAGGATTTAGCAAAATTGAACTTTCAAACGATG 681

Qy 223 ThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGluAspIleAlaGln 242
Db 682 TTACAACCAGCATCATTAGTAATACGACTGCCGAAATTATGCCCAAGAGGCAATTCAAGCG 741

Qy 243 LeuLeuThrArgGlnValLysGluProValArgPheTyrGluSerIleGlyValMetGln 262
Db 742 CAAATTCCTGTCATTAGTAATACGACTGCCGAAATTATGCCCAAGAGGCAATTCAAGCG 861

Qy 263 GluAlaGlyIleSerAsnPheIleGluLeuGlyProGlyLysValLeuSerGlyPheVal 282
Db 802 GCTATGACGTAGGAACCATGATTGAAGTTGGTCCAGGGAAAACATTAACTGGTTTTGTT 801

Qy 283 LysLysIleAspGlnThrAlaHisLeuAlaHisValGlnAspGlnAlaSerLeuValAla 302
Db 862 AAAAAAATTGACAAAACAATTGAAATGCACACCGTGTGGAAGATGTTGCACATTAACAGAA 921

Qy 303 LeuLeu 304
Db 922 ACGTTA 927

RESULT 9
US-09-134-000C-1582
; Sequence 1582, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1582
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1582

Alignment Scores:
Pred. No.:
Score: 1.48e-85
Percent Similarity: 937.00
Best Local Similarity: 75.17%
Query Match: 61.92%
DB: 61.73%

US-09-308-397-2 (1-306) x US-09-134-000C-1582 (1-948)

Qy   3 LysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArgAspPhe 22
Db 22 AAAACAGCGATTTTATTTGCAGGACAAGGAGCCCAGTATCAAGGGGATGGGTGAAGAATTA 81

Qy 23 TyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnAlaValLeuGlyTyr 42
Db 82 TATCACCAAGAAGCCGATTGTTCGGGAAACTTCGATGAAGCAAGTCATATCTTAGGTTAT 141

Qy 43 AspLeuArgTyrLeuIleAspThrGluLeuAspLysLeuAsnGlnThrArgTyrThrGln 62
Db 142 GAGATGCAGAACTTTGTTTACTGAAATGAAAATGAAACAGAATATCGCAA 201

Qy 63 ProAlaIleLeuAlaThrSerValAlaIleTyrArgGlyLeuGlnLysGlyLysTyrGln 82
Db 202 CCTGCTATTTTAACAGTCAGTGTCGCATTTTACCGTCTTTTGCAACAAAAGGACTAACG 261

Length: 948
Matches: 187
Conservative: 40
Mismatches: 75
Indels: 0
Gaps: 0

```
Percent Similarity:    75.17%      Conservative:   40
Best Local Similarity: 61.92%      Mismatches:     75
Query Match:           61.73%      Indels:          0
DB:                                Gaps:            0

US-09-308-397-2 (1-306) x US-10-434-665-1582 (1-948)

Qy      3 LysThrAlaPheLeuPheAlaGlyGlnTyrLeuGlyMetGlyArgAspPhe   22
            |||||||  ||||| :|||||||||||||||||||      :::
Db     22 AAAACAGCGATTTTATTTAGTGGACAAGGAGCCCAGTATCAAGGGATGGTGAAGAATTA   81

Qy     23 TyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeuGlyTyr   42
            :::|||||||||||||||| ||||||::||  |||||   :::
Db     82 TATCACCAAGAAGCGATTGTCGGGAAACTTCGATGAAGCAAGTCATATCTTAGGTTAT   141

Qy     43 AspLeuArgTyrLeuIleAspThrGluGluAspLysLeuAsnGlnThrArgTyrThrGln   62
            :::||
Db    142 GAGATGGCAGAACTTGTTTACTGAAAATGAACGTTTAAATGAAACAGAATATACGGCAA   201

Qy     63 ProAlaIleLeuAlaThrSerValAlaIleAlaIleTyrArgLeuLeuGlnGluLysGlyTyrGln   82
            :::||||||||||  ||||||||||||   ||:||
Db    202 CCTGCTATTTTAACAGTCAGTGTGCGCATTTACCGTCTTTTGCAACAAAAAGGACTAACG   261

Qy     83 ProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuLeuValAlaSerGlyAla   102
            :::|||  :::|||||||||||||||
Db    262 CCTGATGTCGTAGCGGGTTTAAGCTTAGGGGAAATCAGTGCTTTGGTTGCCAGCGGGGCT   321

Qy    103 LeuAspPheGluAspAlaValAlaLeuValAlaIleAlaLysArgGlyAlaTyrMetGluGluAla   122
            ||||||||||||||||||||||||||||
Db    322 TTGGCTTTTCAGAAGCCAGTGGCCTTGGTCCAAAAGCCGGTCAGTGACAGCAGAAGCA   381

Qy    123 AlaProAlaAspSerGlyValLysMetValAlaValLeuAsnThrProValGluValIleGlu   142
            :::|||||||||||||||||||||||   :||
Db    382 GCACCACAAGGAACTGGCAAAATGTTGCTTATGAAGCCGTGAAGTAATTGAG   441

Qy    143 GluAlaCysGlnLysGlnLysAlaSerGlyGluGluLeuGlyValValThrProAlaAsnTyrAsnThrPro   162
            :::|||||   |||||||||||||||||||||
Db    442 AAAGCCTGCCAAGAAGCCAGTGCTTCGGAATTGTGGCTCCAGCAAATTATATACACCA   501

Qy    163 AlaGlnIleValIleGluAlaGlyLyGluValValAlaValAlaValAlaValAlaGluValLeuGluLeuGln   182
            ||||||||||||||||||||   :||::  |||||
Db    502 CAACAAAATCGTGATTGGTGGTGAGGTTGCTGCTGTTGATCAAGCGATGACACTTCTCAAA   561

Qy    183 GluAlaCysGlnLysArgLeuIleLeuProLeuLysValSerGlyProPheHisThrAlaLeu   202
            :::|||   :::||||   |||||||||
Db    562 GAAGCTGGTGTGCAGAAAGCGAAGATGATTCCGTTAAATGTGAGTGGCCCCTTTCCATACCGCGCTG   621

Qy    203 LeuGluProAlaSerGlnLysGlnLysLeuLeuAlaGlyThrLeuAlaGlnValSerPheSerAspPhe   222
            |||||||||||||||||   ||||:::::::||
Db    622 TTACAACCAGCATCAAAAAAATTGCTCAGGATTTAGCAAAATTGAACTTTCAAACGATG   681

Qy    223 ThrCysProLeuValGlyAsnThrGluAlaValMetGlnLysGluAspIleAlaGln   242
            :::  |||::||:||:::||
Db    682 GCTATGAACGTAGGAAACGATGATTGAAGTTGGTCAGGGAAAACATTAACTGGTTTTGTT   741

Qy    243 LeuLeuThrArgGlnIleValLysGluProValArgPheTyr:GluSerIleGlyValMetGln   262
            ||||||||||||   ||   :|||
Db    742 TTATTGGAAAAGCAAGTCATGTCGTGCGTACGTTTGAAGACAGTATCGAAACGATGAAG   801

Qy    263 GluAlaGlyIleLeuSerAsnPheIleGluIleLeuGlyProGlyLysValLysSerGlyValPheVal   282
            :::|||
Db    802 GCTATGAACGTAGGAACGATGATTGAAGTTGGTCCAGGGAAAACATTAACTGGTTTTGTT   861

Qy    283 LysLysIleAspAspPhnThrArgAlaHisLeuAlaHisIleValGluAspGlnAlaSerLeuValAlaAla   302
            ||||||||||||:::|||
Db    862 AAAAAAATTGACAAAACAATTGAAATGACCGTGTGGAAGATGTTGCAACATTAACAGAA   921

Qy    303 LeuLeu   304
            |||
Db    922 ACGTTA   927

RESULT 11
US-10-282-122A-15949
```

```
; Sequence 15949, Application US/10282122A
; GENERAL INFORMATION:
;  APPLICANT: Wang, Liangsu
;  APPLICANT: Zamudio, Carlos
;  APPLICANT: Malone, Cheryl
;  APPLICANT: Haselbeck, Robert
;  APPLICANT: Ohlsen, Karl
;  APPLICANT: Zyskind, Judith
;  APPLICANT: Wall, Daniel
;  APPLICANT: Trawick, John
;  APPLICANT: Carr, Grant
;  APPLICANT: Yamamoto, Robert
;  APPLICANT: Forsyth, R.
;  APPLICANT: Xu, H.
;  TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;  FILE REFERENCE: ELITRA.034A
;  CURRENT APPLICATION NUMBER: US/10/282,122A
;  CURRENT FILING DATE:   2003-02-20
;  PRIOR APPLICATION NUMBER: 60/191,078
;  PRIOR FILING DATE: 2000-03-21
;  PRIOR APPLICATION NUMBER: 60/206,848
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 60/207,727
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: 60/230,335
;  PRIOR FILING DATE: 2000-09-06
;  PRIOR APPLICATION NUMBER: 60/230,347
;  PRIOR FILING DATE: 2000-09-09
;  PRIOR APPLICATION NUMBER: 60/242,578
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: 60/253,625
;  PRIOR FILING DATE: 2000-11-27
;  PRIOR APPLICATION NUMBER: 60/257,931
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: 60/267,636
;  PRIOR FILING DATE: 2001-02-09
;  PRIOR APPLICATION NUMBER: 60/269,308
;  PRIOR FILING DATE: 2001-02-16
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 78614
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15949
;  LENGTH: 927
;  TYPE: DNA
;  ORGANISM: Clostridium acetobutylicum
US-10-282-122A-15949

Alignment Scores:
Pred. No.:                1.69e-62          Length:       927
Score:                    710.50            Matches:      146
Percent Similarity:       67.11%            Conservative: 56
Best Local Similarity:    48.50%            Mismatches:   96
Query Match:              46.81%            Indels:        3
DB:                       9                 Gaps:          3

US-09-308-397-2 (1-306) x US-10-282-122A-15949 (1-927)

Qy      3 LysThrAlaPheLeuPheAlaGlyAlaGlyMetGlyAlaGlnTyrLeuGlyMetGlyAspPhe   22
            |||                |::|||||  ||||||| ||   |||
Db      7 AAGATTGCATTTTGTTTTTCAGGACACAGGGTTCCAGTATGTTGGAATGGGAAAGGATCTA   66

Qy     23 TyrAspGlnTyrProLeuValLysGluThrIleAspArgAlaSerArgValLeuValGlyTyr   42
            :::||||||||||||||||||||||  |::|||||   :::
Db     67 TACGATAATTACCAAGACGCAAAGAACTTTTGATAAAGCTGAAGTGCTTCGGCTTT   126

Qy     43 AspLeuArgTyrLeu--IleAspThrGluGluAspLysLeuAsnGlnThrArgTyrThr   61
            :::||   |||   |||
Db    127 AAAATCAGTGAATTATGCTTCGAAGAAAGAATGAAGAATTAAATTTAACTGAGAACACT   186

Qy     62 GlnProAlaIleLeuGluAlaThrSerValAlaIleAlaTyrArgLeuLeu--GlnGluLysGly   80
            :::||  |||::||
Db    187 CAGCCAGCAGTTTTAATTACTAGTATAGCTGCTTTAAGACACTTGAAGAAGAAAAAGGA   246
```

Score: 669.50   Matches: 143
Percent Similarity: 62.71%   Conservative: 47
Best Local Similarity: 47.19%   Mismatches: 110
Query Match: 44.10%   Indels: 3
                                      Gaps: 3
DB:

US-09-308-397-2 (1-306) x US-10-369-493-46809 (1-954)

```
Qy    1 MetThrLysThrAlaPheLeuPheAlaGlyValGlnGlyAlaGlnTyrLeuGlyAlaGlyMetGlyArg  20
        | |:::|   || ||:   ||| :||  :: :|  |||  |:||:|:: |  :||||  :|| ::
Db    1 ATGAGTAAGATTGCATTTTATTCCCGGGTCAGGGATCACAATTTATCGGCATGGGAAAA             60

Qy   21 AspPheTyrAspGlnTyrProIleValThrIleAspPheAlaSerGlnIleAspValLeu           40
        :::          |||:| || |:  ||  ||| ||  ||| : ||||| :|:
Db   61 GAGCTTTATGAGCAGTGCCTGCAAACGGTCTGTTGATGAAGCCGATGAAACGTTG               120

Qy   41 GlyTyrAspLeuArgTyrLeuIle--AspThrGluGluLysLeuAsnGlnThrArg              59
        ::                     :::             ||  |  :|| |||
Db  121 GAAACAAAACTCAGCTGCCTATTTTGAGGGGGATGCTGAAGAATTAACACTTACATAC           180

Qy   60 TyrThrGlnProAlaIleLeuAlaThrSerValAlaIleThrSerValAlaLeuValGlnLeuGlnLys  79
         | | | |  || ||: :| :::   :|:    |::    : |  ::|| || :|  ||| :
Db  181 AATGCCCAGCCTGCTTTGCTTGCGACCAAGCAAGCATCGTGTTCTTGAAAATTAAAGGAGATCT       240

Qy   80 GlyTyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAla            99
         || ||:    :|:  |||  || ||  |||  ::| |||| :| : :|| |||
Db  241 GGCATTACACCTGATTTCACAGGACGACAGCTTGTGAATATTCTGCACTGTTGCG              300

Qy  100 SerGlyAlaLeuAspPheGluValMetGlnLysGlnLysLysGluGluGlyArgGlyAlaTyrMet      119
        :::   || |  |||:  |   ::  |:|: |: | ::    : :| |||| ||
Db  301 GCTGGCGCTCGTGCTTCTTCAAGATGCTGTTTATACTGTCAGAAAGCGCGGAGAGTTTATG         360

Qy  120 GluGluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGlu           139
        :::       |||  | |||  | ::| :|: || :|:  ::|  | :| |:|| :||
Db  361 AATGAAGAGCGGTGCCGGCTGCGGAAGGAGCAATGGCGATCCTCGGCATGCTGATGCTGAA        420

Qy  140 ValIleGluGluAlaCysGlnLysLeuAlaSerGluGluGly--ValValThrProAlaAsn         158
        :::   : :::  | :|:  || :::||: |:  | :    || ||: ::|: || ::|
Db  421 GCATTAAAGCAAGTAACCGATAAAGGTCACAGAGGAGGCAACCTTGTACAGCTTGCGAAT         480

Qy  159 TyrAsnThrProAlaGlnIleValIleGluAlaGlyGluValValAlaValAlaAspArgAlaVal      178
        :::        |  ::| :::| :| :  || ||  : |||:|  ::|  | |:|  ||:
Db  481 CTCAACTGTCCTGGCCAAATCGTCATTCCGGAACAGCTAAGGGGTTGAGCTTGCATCT            540

Qy  179 GluLeuLeuGlnGluAlaAlaLysAlaArgLeuIleProLeuLysValSerGlyProPhe            198
        :::          |:|    || ::|:|||   | :    |: :|::|| |:| :||
Db  541 GAACTGGCAAAAGAAGAACGGCAAAAACCGCAATTCCGCTTGAAGTAAGCGGGTCCGTTC        600

Qy  199 HisThrAlaLeuLeuGluProAlaSerGlnLysGlnLeuGluAlaGluThrLeuAlaGlnValSer      218
         |:|:|  || :|||  |: |   |:|| ::|:  || |  |   :::| || |:  :
Db  601 CATTCTGAACTGATGAAAACCGCTCTGAAAAGTGAAAGAGAGGTTATTGGACGCCGTGTGAC       660

Qy  219 PheSerAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMet--GlnLys            237
        :::   ||   | :| :::    :||  ::|   |  | |   | :||||  || :|
Db  661 ATAAAAGACCGCTGACGTTCCGGTCATCTCAAATGTTCTGCTGACGATGACTGAAAAA          720

Qy  238 GluAspIleAlaGlnLeuLeuThrArgGlnValLysGluProValAlaArgPheTyrGluSer        257
        :::         |  :| |  | | |  |: ::  | |  ||  |: :  |   :| |
Db  721 GCAGATATCAAAGAAAAAACTTATTGAGCAGTTTACTCTCCGGTTCGTTTTGGAGAAAGC        780

Qy  258 IleGlyValMetGlnGluAlaGlyIleSerAsnPheIleGlyIleGluGlyProGlyLysVal         277
        :::         |  ::|   || ||  :|    |    |     |  |  |: |:|:|
Db  781 ATTACAAGCTGATCGACGAGGGTTACGACTTTTATTGAAATCGTCGGAAAAAGTG              840

Qy  278 LeuSerGlyPheValLysLysIleAspAsnThrAlaHisLeuAlaHisValGluAspGln           297
        :::          |:| :||  ||    | | | |   |  | | :|| | |  ||
Db  841 CTTTCAGGCCTTGTGAATATTCTGAATAACAATTGCTGTATCAGATCCG                    900

Qy  298 AlaSerLeu     300
        :::  |::
Db  901 GAAACGATC    909
```

RESULT 13

```
Qy   81 TyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuValAlaSer          100
        ::: ::|   :||:  |||  || ||  ||  || |||| :| : :|| ||| |:
Db  247 ATAAAACCTGATGTTGTTGCAGGTCTTAGCCTGGGAGAATTCTGCACATGTTGCAGT           306

Qy  101 GlyAlaLeuAspPheGluValMetGlnLysGlnLysLysGluGluGlyArgGlyAlaTyrMetGlu     120
        :::   || |  |||   |  ::  |:|: |: | ::    : :|  |  || |||
Db  307 GGGAGTTTTCATTGAGGATGCAGTAAGAGTTGATGAAGAGAAGGAAGATATATGCAA          366

Qy  121 GluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProValGluVal          140
        ::|       |||  | |||  | ::| :|: || :|:  ::|  | :| |:|| :||||
Db  367 GAAGCAGCAGTACCAAAAGGAATAGGTACTACATGGCTCTATAATCGGACCTGAGGTGATGTA       426

Qy  141 IleGluGluAlaCysGlnLysSerGlnLysLysAlaSerGluLeuValValThrProAlaAsnTyrAsn  160
        ::|   : :::  | :|:  ||   | ::  |::   | | | ::|  |:|: || ::|:::
Db  427 GTTAGAGAGTGCGCTGAGCAATCAAAAGAAAGGAATAGTAGAGTAGCAAATTATAAT            486

Qy  161 ThrProAlaGlnIleValIleAlaGlyGluValValAlaValAlaAspArgAlaValGluLeu        180
        |:|        |  ::| :::| | ||  : |||:|  ::|  | |:|  ||:  :::
Db  487 TGTCCAGGACAAATTGTTATAGCGGAGGAAGTTAAAGCTGTTGCAGATAGGGCCCTACTAAG        546

Qy  181 LeuGlnGluAlaAlaLysAlaArgLeuIleProLeuLysValSerGlyProPheHisThr          200
        :::          |:|    || ::|:|||   | :    |: :|::|| |:| :||  | |
Db  547 TTAAAGGAAGCCGGAGCAAGAAACAGTAAATGCTTTCAGTAAGTGGACCATTTCACACA        606

Qy  201 AlaLeuLeuGluProAlaSerGlnLysLeuGluAlaGluThrLeuAlaGlnValSerPheSer        220
        :::         |: |   |:|| ::|:  |  |   :::| || |:  :   :::
Db  607 TCTATGCTGAACTGTCTGAAAAATTAGAAGAAGATATAAAATATAAAATATAGAA               666

Qy  221 AspPheThrCysProLeuValGlyAsn--ThrGluAlaAlaValMetGlnLysGlnLysLysGluAsp   239
        :::   | :| :::    :||  ::| || |  | |   | :||| :::|: | ::
Db  667 GATATGAAGGTACCAGTTATTACAAATGTAACCAGAGGAGACTATGTGTAGAGATAAGGATCAG       726

Qy  240 IleAlaGlnLeuLeuThrArgGlnValLysGluProValAlaArgPheTyrGluSerIleGly       259
        :::         |  :| |  | | |  |: ::  | |  ||  |: :  |   :| | ::|
Db  727 ATAAAAAGGTTTATTGAAAAAGCAAGTCATGAGCTCTGTTAGATGGGAAGATACAATAAGA        786

Qy  260 ValMetGlnGluAlaGlyIleSerAsnPheIleGluGlyIleProGlyLysValLeuSer          279
        :::      |  ::|   || ||  :|    :|    |  :  |  |: |:|:|  :::
Db  787 AGAATGATGATGAGTAGGATGATACATTTATAGACGTTGACCAGTGACGTAAGACCTTAAGT        846

Qy  280 GlyPheValLysLysIleAspAspGlnThrAlaHisLeuAlaHisValGluAspGlnAlaSer        299
        :::         |:| :||  ||  |: | | |   |  | | :|| | | | ::: :::
Db  847 TCATTTATAAAGAAAAATAAATGACTATATTTAATATTGAAAAAGCTGAAGAT               906

Qy  300 Leu     300
        ::: |::
Db  907 TTA    909
```

RESULT 12

US-10-369-493-46809
; Sequence 46809, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 46809
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-10-369-493-46809

Alignment Scores:
Pred. No.:   2.62e-58   Length: 954

Qy   80 GlyTyr---GlnProAspMetValAlaGlyGluSerLeuGlyGluTyrSerAlaLeuVal 98
          |||||| :::|||||||||||
Db   256 GGTTCTTGAGCAACCTGCGGTTTAGCTGGTCACAGCTGGGTGAATATTCAGCACTGGTA 315

Qy   99 AlaSerGlyAlaLeuAspPheGluAspAsnGlnAlaValAlaLeuValAlaLysArgGlyAlaTyr 118
          :::|||||||| ::::|||||
Db   316 TGTGCGGGCGTGATTGATTTAAACAAGCATCAAGCCTGGTTGAGCTGGTCAATTG 375

Qy   119 MetGluGluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProVal 138
          ||| :::||| ||||
Db   376 ATGCAACAAGCGGTGCCTGCCCGGTACGGGTGCAATGTACGCGATCATCGGTCTAGAAGAT 435

Qy   139 GluValIleGluGluAlaCysGlnLysLysAlaSerGluGluGlyValValThrProAlaAsn 158
          ||| ::|||||
Db   436 GAAGGCGATTGCTAAAGCCTGCTGACGCGGCCAAGGTGAAGTGGTTTCTCCTGTAAAC 495

Qy   159 TyrAsnThrProAlaGlnIleValIleAlaGlyLysValAlaAlaValAlaAspArgAlaVal 178
          ::|||||||| ::||||||
Db   496 TTTAACTCACCAGGCCAAGTGGTTATTGCTGGTCAAAAAGATGCGGTTGACGTGCGGGC 555

Qy   179 GluLeuLeuGlnGluAlaGlyAlaLysGlyArgLeuIleProLeuLysValSerGlyProPhe 198
          :::||||||||| ||||||
Db   556 GTTCTGTGTAAAGAAGCGGGCGCGAAACGTGCGCTGCCTGCCAGTTTCCGTACCATCA 615

Qy   199 HisThrAlaLeuLeuGluProAlaSerGlnLysLysLeuAlaGluThrLeuAlaGlnValSer 218
          ||| ::||||| :::||||||
Db   616 CACTGCGCGTTGATGAGCCTGCCGATGAATTGGCAAAAACTCTAGCAGAGCTTGAA 675

Qy   219 PheSerAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValMetGlnLysGlu 238
          ||| :::|||
Db   676 TTCAATGCACCACAAATTCCGGTCATCAATAACGTTGAT------GTTGTGGCTGAAACG 729

Qy   239 Asp-------IleAlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyr 255
          ||| ||||||
Db   730 GATCCGGTAAAAATTAAAGATGCGTTGATTCGTCAACTCATAGCCCAGTTCGTTGGACT 789

Qy   256 GluSerIleGlyValMetGlnGlnAlaGlyValIleSerAsnPheIleGlyLeuGlyProGly 275
          :::
Db   790 GAATGCCTTGAACAAATGAGCGCACAAGGTGTCGAAAAGCTGATTGAAATGGGGCGGGT 849

Qy   276 LysValLeuSerGlyPheValLysLysIleAspGlnThrAlaHisLeuAlaHisLeuValGlu 295
          |||||||| ::::|||
Db   850 AAAGTATTGACTGGTCTAACAAAACGTATTGTAAAAACCCTAGAAGGTGTCGCAGTCAAT 909

Qy   296 AspGlnAlaSerLeuValAlaLeu 303
          :::||||||
Db   910 GACGTGGCTTCTTTGGATGCGGTG 933

RESULT 14
US-10-369-493-41012
; Sequence 41012, Application US/10369493
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
;
; SEQ ID NO 41012
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Bacillus halodurans
US-10-369-493-41012

Alignment Scores:

US-10-282-122A-41191
; Sequence 41191, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 41191
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Vibrio cholerae
US-10-282-122A-41191

Alignment Scores:
Pred. No.:   4.29e-57
Score: 657.50
Percent Similarity: 66.23%
Best Local Similarity: 47.40%
Query Match: 43.31%
DB:

Length: 939
Matches: 146
Conservative: 58
Mismatches: 97
Indels: 7
Gaps: 4

US-09-308-397-2 (1-306) x US-10-282-122A-41191 (1-939)

Qy   1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlnTyrLeuGlyMetGlyArg 20
         |||||| :||||
Db   16 ATGAGTAAGTTTGCTATCCTATTTCCAGGTCAGGGCTCGCAAGCAGTAGGTATGCTGGCT 75

Qy   21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu 40
         :::|||||||| ||||||
Db   76 GACCTTGCCGAGCAGTATGCTGTGGTAAAACAAACATTCGCCGAAGCTTCAGAAGTGCTT 135

Qy   41 GlyTyrAspLeuArgTyrLeuIle--AspThrGluGluAspLysLeuAsnGlnThrArg 59
         ||||||||||| :::||
Db 136 GGTTACGATCTGTGGCGGTCGTTGGTCAAGATGGCCCTGTGGAAGATCTCAACCAAACTTTC 195

Qy   60 TyrThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLys 79
         ||| ||:::
Db 196 CGTACTCAACCTGCGGTTGCTTGCCCTCTGTTGCGATTTGGCGTGTATGGCAGCAACTG 255

```
Pred. No.:              9.78e-57        Length:         942
Score:                  654.00          Matches:        141
Percent Similarity:     64.40%          Conservative:    58
Best Local Similarity:  45.63%          Mismatches:     106
Query Match:            43.08%          Indels:           4
DB:                                     Gaps:             4

US-09-308-397-2 (1-306) x US-10-369-493-41012 (1-942)

Qy    1  MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg   20
            ||||||||||||::|||      :::|||||||
Db    1  ATGGCAAAAGTAGCATTTCTATTCCCAGTCACAGTCTGTCGGGCATGGGGAGC           60

Qy   21  AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu   40
            :::                          :::
Db   61  GAATTACTTTCGAGGAGAAAA---GCAAAAAGAGATTTTTGACGAGGCGGATGAAAGACTC  117

Qy   41  GlyTyrAspLeu--ArgTyrLeuIleAspThrGluGluLysLeuAsnGlnThrArg        59
            |||          :::                  ::|||
Db  118  GGCCATTCCCTTTCAAGCATTATGTTGAAGGGCCAGAGAGAAAAATTGCGCCGGACGGAA  177

Qy   60  TyrThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLys   79
            :::|
Db  178  AATACGCAACCGGCCTTGTTGACGATGAGCACGGCCGTTTATCGCTTCGTGCGTGAATAT  237

Qy   80  GlyTyrGlnProAspMetValAlaGlyTyrLeuSerLeuGlyGlyTyrSerAlaLeuValAla   99
            ::|||||                  |||||
Db  238  GGAATCAAACCTGATTATACAGCCGGTCATAGTCTAGGGGAGTACAGTGCCCCTTGTGGCT  297

Qy  100  SerGlyAlaLeuAspPheGluAspGlnAlaValAlaLeuAlaLysArgGlyAlaTyrMet  119
            :::|||
Db  298  TCAGGCTCTTAACGTTTGCCGATGCTGTGTACGCTGGTCATCACCGGGATTGTTTATG  357

Qy  120  GluGluAlaAlaProAlaAspSerGlyLysMetValAlaValAlaLeuAsnThrProValGlu  139
            ||||||||
Db  358  GAAGAGGCGGTACCCATTCGGCAAGGAGCAATGGCTGCCATCCTTGCATGGAGCGGGAC  417

Qy  140  ValIleGluGluValAlaCysGlnLysAlaSerGluLeuGly--ValValThrProAlaAsn  158
            :::||
Db  418  GAATTAGAACAAGTAGCAAGGAGCGCGTAACAGAGACAGGAGCCTGTCGTTGGTCAAAC  477

Qy  159  TyrAsnThrProAlaGlnIleValIleValAlaAlaGlyTyrGluValValAlaValAlaAspArgAlaVal  178
            :::||||
Db  478  TTAAACTGTCCTGGACAAATTGTCATCTCAGGTTCTGCTGAGGGTGTCGAACAAGCATCA  537

Qy  179  GluLeuLeuGlnGluLeuGlnProAlaLeuGlyIleProLeuLysValSerGlyTyrProPhe  198
            ::|
Db  538  GAGGAAGCAAAGGAAGCAGGGGGAGTGATCCCATTGCCAAGTGAGCCGGACCGTTT      597

Qy  199  HisThrAlaLeuLeuGluProAlaSerGlnLysLeuAlaGlyThrLeuAlaGluThrLeuValSer  218
            |||||
Db  598  CATTGACATTCGCTCATCTCATTGACCAAGTGTACTCTCCAGTTCGTTCGGTGGGGACACT  657

Qy  219  PheSerAspPheThrCysProLeuValGlyAsnThrGluAlaAlaValAlaMetGlnLys--  237
            :::||||
Db  658  GTTCGTCGCATGCTTGAGCTCGGAGTCGGATCAGGAAATGTG                    717

Qy  238  GluAspIleAlaGlnLeuLeuThrArgGlnValLysGluProValArgPheTyrGluSer  257
            ||||
Db  718  GCTGACATTCGCTCATCTCATTGACCAAGTGTACTCTCCAGTTCGTTCGGTGGGGACACT  777

Qy  258  IleGlyValMetGlnGluAlaGlyIleSerAsnPheIleGluIleGlyProGlyLysVal  277
            :::|
Db  778  GTTCGTCGCATGCTTGAGCTCGGAGTCGGATCAGGAAATGTG                    837

Qy  278  LeuSerGlyPheValLysLysIleAspSerGlnThrAlaHisLeuAlaHisValGluAspGln  297
            |||||
Db  838  CTCTCAGGCTCCGTCCGCAAGCTACAGCCGCCGGTTAATGTTTTTGTGAGTGATCGG     897

Qy  298  AlaSerLeuValAlaLeuAlaLeuGluLys  306
            ||||
Db  898  GCAAGCATTGAAGGCGGATGTAAAAAAA  924
```

RESULT 15
US-10-282-122A-32186
; Sequence 32186, Application US/10282122A
; GENERAL INFORMATION:
;   APPLICANT: Wang, Liangsu
;   APPLICANT: Zamudio, Carlos
;   APPLICANT: Malone, Cheryl
;   APPLICANT: Haselbeck, Robert
;   APPLICANT: Ohlsen, Kari
;   APPLICANT: Zyskind, Judith
;   APPLICANT: Wall, Daniel
;   APPLICANT: Trawick, John
;   APPLICANT: Carr, Grant
;   APPLICANT: Yamamoto, Robert
;   APPLICANT: Forsyth, R.
;   APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32186
;   LENGTH: 930
;   TYPE: DNA
;   ORGANISM: Proteus mirabilis
US-10-282-122A-32186

Alignment Scores:
Pred. No.:   2.76e-56   Length: 930
Score: 649.50   Matches: 145
Percent Similarity: 63.84%   Conservative: 51
Best Local Similarity: 47.23%   Mismatches: 108
Query Match: 42.79%   Indels: 3
DB: Gaps: 3

US-10-282-397-2 (1-306) x US-10-282-122A-32186 (1-930)

Qy   1 MetThrLysThrAlaPheLeuPheAlaGlyGlnGlyAlaGlnTyrLeuGlyMetGlyArg   20
            |||||||||||||::||| :::|||||||
Db   1 ATGACTGATTTTGCAATGGTTTTCCCTGACAGGGATCACAGGGATCAAAGCCATTGGCA   60

Qy   21 AspPheTyrAspGlnTyrProIleValLysGluThrIleAspArgAlaSerGlnValLeu   40
            :::   :::
Db   61 GAACTTGCCGAGCCATCATCCAATAGTGACAGAAACATTTGCTCAAGCATCTGATGATATTG 120

Qy   41 GlyTyrAspLeuArgTyrLeuIleAspThr---GluGluLysLeuAsnGlnThrArg   59
            |||::|
Db 121 GGTTATTCCTTTGGATTTAGTGCAAAAGGTCCTGAGGAGAAGTTAAAACAAACATG   180

Qy   60 TyrThrGlnProAlaIleLeuAlaThrSerValAlaIleTyrArgLeuLeuGlnGluLys   79
            :::::|||||
Db 181 ... (continued)

```
Db  181  AAAACACAGCCGGCATTATTAGCAGCATCCGTTGCTATTTGGCGAGTATGGCAAGAAAAA  240
                  |||||||||||||||||:::|||| ||||||||||||||||||||:|||
Qy   80  ---GlyTyrGlnProAspMetValAlaGlyLeuSerLeuGlyGluTyrSerAlaLeuVal   98
              ||| ||||||:::||||| ||||||||||||||||||||:|||
Db  241  CAAGGCAAAATGCCACAAATGATGGCAGGTCACAGTCTTGGTGAGTATTCTGCTTAGTC  300

Qy   99  AlaSerGlyAlaLeuAspPheGluAspAlaValAlaLeuValAlaLysArgGlyAlaTyr  118
              :::|||| :::|||||||||||||||||||||||||||||| ||||
Db  301  TGTGCTGGCGTAATTGATTTGCTGCGGCGATTAAACAGTAGAATTGCGCGGTCAATTA  360

Qy  119  MetGluGluAlaAlaProAlaAspSerGlyLysMetValAlaValLeuAsnThrProVal  138
              |||||||||| ||||||||||| :::||| ||| |:::||||
Db  361  ATGCAAGAGGCTGTACCTGCAGGTACTGGCGCCATGTATGCAATTATCGGATTAGATAAT  420

Qy  139  GluValIleGluGluValCysGlnLysAlaSerGluLeuGlyValValThrProAlaAsn  158
              :::|||||||||||||||||||||||:::||||||:::|||||||||
Db  421  GATGCTATTCGAAAAGCTTCGTGAAGATGCGGCTCAAGGACAAGTTGTCTCACCTGTGAAC  480

Qy  159  TyrAsnThrProAlaGlnIleValIleAlaGlyGluValValAlaValAlaAspArgAlaVal  178
              :::|||||:::||||||||| :::||||||||||||:::||||||||||
Db  481  TTTAACTCACCCGGTCAAGTGGTGATTGCGGGTAATAAAGAAGCCGTAGAGCCGTGCAGGG  540

Qy  179  GluLeuLeuGlnGluGlyAlaAlaLysArgLeuIleProLeuLysValSerGlyValProPhe  198
              ||| :::|||||| ||||||||:::|||||||||||
Db  541  GCATTATGTAAAGAGCTGAGCGAAACGTGCGTTACCTTAGCGGTAGTGTGCCTTCT  600

Qy  199  HisThrAlaLeuLeuGluProAlaSerGlnLysGlnLysLeuAlaGlnThrLeuAlaGlnValSer  218
              ||||||||||||||:::||| ||:::||||| ||||||||||||:::|||
Db  601  CACTGTGCTTTAATGAAGCCTGCTGCAGATAAGTTAGCTGTTGCATTGCAAGAAATTGAA  660

Qy  219  PheSerAspPheThrCysProLeuValGlyAsnThrGluAla---AlaValMetGlnLys  237
              :::|||||||||||||||:::||| ||| |||||||||
Db  661  TTTAAACAACCTGAAATTCAAGTTGTTAATAAATGTTGATGTGAAAGCACAAACCGATGCT  720

Qy  238  GluAspIleAlaGlnLeuLeuThrArgGlnValLysGlnValProValArgPheTyrGluSer  257
              |||||||||||||||||||||||:::|||||||||:::|||||||||
Db  721  AATGCTATTCGAGATGCATTAGTTCGTCGTCAGCTTTATAAACCAGTCCGCTGGAAACG  780

Qy  258  IleGlyValMetGlnGluAlaGlyIleLeuSerAsnPheIleGluIleLeuGlyProGlyLysVal  277
              :::||||||||||||||||||||||:::|||||||||||||||||||
Db  781  GTTGAATTATTGCTGGTAAGGGCATCACACAATTATTAGAAATAGGACCCCGGTAAAGTA  840

Qy  278  LeuSerGlyPheValLysLysIleAspGlnThrAlaHisLeuAlaHisValGluAspGln  297
              ||||||||| :::||| ||| |:::|||||
Db  841  TTAACTGGTTTAACGAAACGTATTTCTAAAGAGATGAACGCTGCAGCAGTAATGATATT  900

Qy  298  AlaSerLeuValAlaLeuLeu  304
              ||||||||||| |||
Db  901  GCATCATTAGACGCTGCATTA  921
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Search completed: June 11, 2003, 22:14:11
Job time : 671 secs